

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd

OM protein - protein search, using sw model

```
Run on:      July 29, 2004, 17:37:45 ; Search time 13 Seconds
              (without alignments)
              1718.315 Million cell updates/sec
```

Title: US-10-024-652-2570

Sequence: 1 MAGSGAMKRLKSLMRKDDAP.....LQSYRQEVDRTCANCGSSP 422

Scoring table: BLOSUM62
Gap: 10.0, Gapext: 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

```
Minimum DB seq length: 0
```

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match 0%
	Maximum Match 100%

Database : SwissProt_42:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Length	DB	ID	Description
1	2179	99.8	429	1	ZNT4_HUMAN	O14863 homo sapien
2	2016.5	92.4	430	1	ZNT4_MOUSE	O35149 mus musculi
3	1990.5	91.2	430	1	ZNT4_RAT	O55174 rattus norv
4	747	34.2	359	1	ZNT2_RAT	O82941 rattus norv
5	642	29.4	388	1	ZNT3_MOUSE	P97441 mus musculi
6	616	28.2	388	1	ZNT3_HUMAN	O99728 homo sapien
7	386	17.7	313	1	ZITB_ECOLI	P15757 escherichia
8	385	17.6	311	1	ZITB_ECOS7	O8x400 escherichi
9	376	17.2	312	1	ZITB_SALTY	O8zq3 salmonella
10	372	17.0	312	1	ZITB_SALTY	O8z8b6 salmonella
11	355	16.3	312	1	ZITB_YERPE	O82956 yersinia p
12	353	16.2	316	1	CCCD_ALSCP	P31512 alcaligenes
13	353	15.2	316	1	CCCD_ALSCP	P41177 alcaligenes
14	343	15.7	436	1	COT1_YEAST	P32798 saccharomy
15	342	15.7	442	1	ZRC1_HUMAN	P20107 saccharomy
16	289	13.2	507	1	ZNT1_HUMAN	O9y6m5 homo sapien
17	284.5	13.0	507	1	ZNT1_RAT	O6z720 rattus norv
18	283.5	12.9	503	1	ZNT1_MOUSE	O6z738 mus musculi
19	230	10.5	732	1	YMH3_GCHPO	O9tfc3 schistosac
20	218	10.0	30	1	YMH3_BOVIN	O9tfc3 schistosac
21	185	8.5	108	1	YGLB_BACST	P35540 bacillus s
22	171.5	7.9	283	1	Y449_METJA	O57891 methanococ
23	160.5	7.4	290	1	YEAB_BACVU	P46348 bacillus s
24	148.5	6.8	310	1	YCG3_SYNY3	P74068 synechocys
25	137.5	6.3	251	1	YOR5_XANX3	O99308 caenorhabd
26	136.5	6.3	510	1	YMH3_YEAST	O93278 saccharomy
27	117.5	5.4	549	1	SMF2_YEAST	P38778 saccharomy
28	107	4.9	567	1	YFCW_ECOLI	P52138 escherichi
29	107	4.9	1032	1	Y895_HAEIN	O57124 haemophilu
30	105.5	4.8	1286	1	IRBP_BOVIN	P16661 bos taurus
31	103	4.7	301	1	P34_RICRI	O21559 rickettsia
32	100	4.6	309	1	REC3_MOUSE	O8b123 mus musculi
33	100	4.6	547	1	YUDB_SALTY	P36555 salmonella

45	95	4.4	502	1	NU2C_ME5V1	Osmu6	mesotigma
44	95	4.4	314	1	PFDV_ECOLI		
43	96	4.4	366	1	PF2R_MOUSE		
42	96	4.4	300	1	P34_RICP1		
41	96.5	4.4	1205	1	PD55_SCHPO		
40	97	4.4	705	1	WMLD_STRCO		
39	97.5	4.5	957	1	CLU3_RAT		
38	99	4.5	214	1	SP2M_EAGSU		
37	97.5	4.5	956	1	SP2M_EAGSU		
36	99	4.5	532	1	CLU3_HUMAN		
35	99	4.5	378	1	SATT_MOUSE		
34	99.5	4.6	956	1	CLU3_MOUSE		
33	99	4.6	378	1	CLU3_MOUSE		
32	99	4.6	378	1	CLU3_MOUSE		
31	99	4.6	378	1	CLU3_MOUSE		
30	99	4.6	378	1	CLU3_MOUSE		
29	99	4.6	378	1	CLU3_MOUSE		
28	99	4.6	378	1	CLU3_MOUSE		
27	99	4.6	378	1	CLU3_MOUSE		
26	99	4.6	378	1	CLU3_MOUSE		
25	99	4.6	378	1	CLU3_MOUSE		
24	99	4.6	378	1	CLU3_MOUSE		
23	99	4.6	378	1	CLU3_MOUSE		
22	99	4.6	378	1	CLU3_MOUSE		
21	99	4.6	378	1	CLU3_MOUSE		
20	99	4.6	378	1	CLU3_MOUSE		
19	99	4.6	378	1	CLU3_MOUSE		
18	99	4.6	378	1	CLU3_MOUSE		
17	99	4.6	378	1	CLU3_MOUSE		
16	99	4.6	378	1	CLU3_MOUSE		
15	99	4.6	378	1	CLU3_MOUSE		
14	99	4.6	378	1	CLU3_MOUSE		
13	99	4.6	378	1	CLU3_MOUSE		
12	99	4.6	378	1	CLU3_MOUSE		
11	99	4.6	378	1	CLU3_MOUSE		
10	99	4.6	378	1	CLU3_MOUSE		
9	99	4.6	378	1	CLU3_MOUSE		
8	99	4.6	378	1	CLU3_MOUSE		
7	99	4.6	378	1	CLU3_MOUSE		
6	99	4.6	378	1	CLU3_MOUSE		
5	99	4.6	378	1	CLU3_MOUSE		
4	99	4.6	378	1	CLU3_MOUSE		
3	99	4.6	378	1	CLU3_MOUSE		
2	99	4.6	378	1	CLU3_MOUSE		
1	99	4.6	378	1	CLU3_MOUSE		

ALIGNMENTS

	RESULT 1		
ID	ZNT4_HUMAN	STANDARD;	PRT; 429 AA.
AC	O14863:		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Zinc transporter 4 (Znt-4).		
GN	SLC30A4 OR ZNT4.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fetal brain;		
RX	MEDLINE=98016412; PubMed=9354792;		
RA	Huang L., Gilechier J.;		
RT	"A novel gene involved in zinc transport is deficient in the lethal milk mouse."		
RL	Nat. Genet. 17:292-297(1997).		
CC	-1- FUNCTION: Probably involved in zinc transport out of the cytoplasm. May be by sequestration into an intracellular compartment.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Localised in endosomal vesicle membrane (Probable).		
CC	-1- DOMAIN: Contains a histidine-rich region which is a ligand for zinc and an aspartate-rich region which is a potential ligand for zinc (By similarity).		
CC	-1- SIMILARITY: Belongs to the cation diffusion facilitator family of transporters (CDF, TC 2.A.4). SLC30A subfamily.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way commercialized and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sdb.ch/announce) or send an email to license@isb-sdb.ch .		
CC	-----		
DR	EMBL; AF025409; AAB82561.1; -		
DR	Genew; HGNC:11015; SLC30A4.		
DR	MIM; 602095; -		
DR	GO; GO:0005385; F:zinc ion transporter activity; TAS.		
DR	InterPro; IPR002524; Cation efflux.		
DR	Pfam; PF01545; Cation efflux; 1.		
DR	TIGRFAMs; TIGR01297; CDF; 1.		
KW	Zinc transporter; Transport; Transmembrane; Multigene family.		
FT	DOMAIN 1 113	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 114 134	POTENTIAL.	
FT	DOMAIN 115 113	VACUOLAR (POTENTIAL).	
FT	TRANSMEM 115 113	POTENTIAL.	
FT	TRANSMEM 144 164	POTENTIAL.	
FT	DOMAIN 144 164	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 165 178	POTENTIAL.	
FT	TRANSMEM 179 199	POTENTIAL.	
FT	DOMAIN 200 216	VACUOLAR (POTENTIAL).	
FT	TRANSMEM 217 237	POTENTIAL.	

	ZNT4_MOUSE		PRT;	430 AA.
CC	ID_ZNT4_MOUSE	STANDARD;		
CC	O35149; O35154;			
CC	30-MAY-2000 (Rel. 39, Created)			
CC	30-MAY-2000 (Rel. 39, Last sequence update)			
CC	15-MAR-2004 (Rel. 43, Last annotation update)			
CC	Zinc transporter 4 (Znt-4) (lethal milk protein).			
CC	SLOC0A4 OR ZNT4 OR LM.			
CC	Mus musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Metacera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
CC	NCBI_Taxid=10090;			
CC	[1]			
CC	SEQUENCE FROM N.A.			
CC	STRAIN=C57BL/6, and B6/CBAF1; TISSUE=Brain;			
CC	MEDLINE=98016412; Pubmed=9354792;			
CC	Huang L., Gletschler J.;			
CC	"A novel gene involved in zinc transport is deficient in the lethal			
CC	milk mouse.";			
CC	Nat. Genet. 17:292-297(1997)."			
CC	-I- FUNCTION: Probably involved in zinc transport out of the			
CC	cytoplasm, may be by sequestration into an intracellular			
CC	compartment.			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein. Localized in			
CC	endosomal vesicle membrane (Probable).			
CC	-I- TISSUE SPECIFICITY: Widely expressed. Highly expressed in the			

Query Match	92.4%;	Score 20.6.5;	DB 1;	Length 430;
Best Local Similarity	92.3%;	Pred. No. 7.1e-150;		
Matches 397;	Conservative 14;	Mismatches 16;	Indels 3;	Gaps 2;
QY	1	MAGSGAMKRLKSMRLKRDAPLPLNDTSAFDFDEADEGLSRPNKLRVVVADGSEAPER	60	
Db	1	MAPPGAMKRLKSLRLKDDTPPLPLNDTSADDFSEVDEGLSRPNKLRVVVADDDSEAPER	60	
QY	61	PVNGAAPTLCQADDSSLDDDLPLNTSGLSLKYDSCNCKOREILLKORVYKRLTAAVL	120	
Db	61	PVNGAAPTALQADDSSLDDDLPLNTSGLSLKMDPCNCKREELLKORVYKRLTAAVL	120	
QY	121	YLLFMTEGELVGYIANSIAIMTDALHMLTDLASIIITLLALWLSKSPTRKFTFGFHRL	180	
Db	121	YLLFMTEGELVGYIANSIAIMTDALHMLTDLASIIITLLALWLSKSPTRRFTFGFHRL	180	
QY	181	VLSAMISVLLVYTLINGEFLLEYAOFETIHNHYEINDIMILITAAVGAANVIMGFLINOSG	240	
Db	181	VLSAMISVLLVYTLINGEFLLEYAOFRTIHNHYEINDIMILITAAVGAANVIMGFLINOSG	240	
QY	241	HRHS--HSHSLPSNPTRGSGCERNHGODSLAVRAAFVHALGDIVQSVGLTAAVITREK	298	

FT	DOMAIN	135	143	VACUOLAR (POTENTIAL) .
FT	TRANSSEM	144	143	POTENTIAL.
FT	DOMAIN	165	178	CYTOPLASMIC (POTENTIAL) .
FT	TRANSSEM	179	199	POTENTIAL.
FT	DOMAIN	200	216	VACUOLAR (POTENTIAL) .
FT	TRANSSEM	217	237	POTENTIAL.
FT	DOMAIN	238	275	CYTOPLASMIC (POTENTIAL) .
FT	TRANSSEM	276	296	POTENTIAL.
FT	DOMAIN	297	311	VACUOLAR (POTENTIAL) .
FT	TRANSSEM	312	332	POTENTIAL.
FT	DOMAIN	333	430	CYTOPLASMIC (POTENTIAL) .
FT	DOMAIN	17	96	ASP-RICH (ACIDIC) .
FT	DOMAIN	241	249	HIS-RICH.
SQ	SEQUENCE	430 AA;	47702 MM;	F34CED3FA4F05FB CRC64;

	Query Match	91.2%	Score 1990.5	DB 1	Length 430
Best Local Similarity	90.7%	Pred. No. 7.6e-148			
Matches 390	Conservative 19	Mismatches 18	Indels 3	Gaps 2	

QY	1	MAGSGAMRRLKSMRKODA	PELNDTSAFDESDGEGSLSPFNKLRYVVDGGEADER	60
Db	1	MAGPAMRRLKSLRKDDAPL	FNDTSAFDFLDEVSDEGLSRFNKLRYVVDGGEADER	60
QY	61	PVNGAHPTLQADDSDILDDPL	PLTNSQLTVSDGDCNCSKOREILKQRYARLITAAVL	120
Db	61	PVNGAHPALQADDSDILDDPL	PLTNSQLTMDPCDNCSSKREILKQRYARLITAAVL	120
QY	121	YLLEWIGELVGGYIANSIAI	WTDAIMLTDLSAIIITLLAAMLSSKSPTRRTPGFHRL	180
Db	121	YLLEWIGELVGGYIANSIAI	WTDAIMLTDLSAIIITLLAAMLSSKSPTRRTPGFHRL	180
QY	161	VLASNIATVLAYIIMLGE	LLAEVQGTIMNNEINGIDIMLITAAVAVANVINGFLINOSG	240
Db	161	VLASNIATVLAYIIMLGE	LLAEVQGTIMNNEINGIDIMLITAAVAVANVINGFLINOSG	240
QY	241	HRHS--HSHSLPSN	SGPTGRSGCERNHGDSTLAVRAAFYHALGDIVQSVGLIAAYIRPK	298
Db	241	HHHSIAHSHSLPSN	SPSNVSS--GSHGQDSTLAVRAAFYHALGDIVQSVGLIAAYIRPK	299
QY	299	PEYKIADPICTYVFS	LVAFTFRILIMDTVTIILEGVPSHLNVDIKELMKLIEDVYSVE	358
Db	300	PEYKIADPICTYFIS	LVAFTFLRIIMDTVTIILEGVPSHLNVDIKESIMKIEDVYSVE	359
QY	359	DINISLISGKSTALVH	QIOLIPGSSSKKEEYOSKXNHILMTFFGYRCTLOLQSYRQEV	418
Db	360	DINISLISGKSTALVH	QIOLIPGSSSKKEEYOSKXNHILMTFFGYRCTLOLQSYRQEV	419
QY	419	RTCANCOSSS	428	
Db	420	RTCANCOSSS	429	

RESULT 4

ZNT2	RAT	STANDARD;	PRT;	359	AA.
AC	Q62961;				
DT	30-MAY-2000 (Rel. 39,	Created)			
DT	30-MAY-2000 (Rel. 39,	Last sequence update)			
DT	15-MAR-2004 (Rel. 43,	Last annotation update)			
DE	Zinc transporter 2 (Znt-2).				
GN	Slc30A2 OR ZNT2.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
NCBI	TaxID=101116;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Sprague-Dawley; TISSUE=Kidney;				
RA	MEDLINE=96203098; PubMed=8617223;				
RA	Palmiter R.D., Cole T.B., Findley S.D.;				
RT	"Znt-2, a mammalian protein that confers resistance to zinc by				
RT	facilitating vesicular sequestration."				
RT	EMBO J. 15:1784-1791(1996).				

```

CC -1- FUNCTION: Involved in accumulation of zinc in endosomal/lysosomal
CC vesicles.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Localized in the
CC membrane of endosomal vesicles (Probable).
CC -1- TISSUE SPECIFICITY: Intestine, kidney, seminal vesicles and
CC testis.
CC -1- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC transporters (CDF, TC 2.A.4). SLC30A subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U50927; AAB02775.1; -.
CC RefSeq; S70632; S70632.
CC InterPro; IPR002524; Cation_efflux.
CC Pfam; PF01545; Cation_efflux; 1.
CC TIGRFAMs; TIGR01297; CDF; 1.
CC Zinc transport; Transport; Transmembrane; Multigene family; Repeat.
CC K01
CC DOMAIN 1 56 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 57 77 POTENTIAL.
CC DOMAIN 78 86 VACUOLAR (POTENTIAL).
CC TRANSSEM 87 107 POTENTIAL.
CC DOMAIN 108 123 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 124 144 POTENTIAL.
CC DOMAIN 145 159 VACUOLAR (POTENTIAL).
CC TRANSSEM 160 180 POTENTIAL.
CC DOMAIN 181 207 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 208 228 POTENTIAL.
CC DOMAIN 229 236 VACUOLAR (POTENTIAL).
CC TRANSSEM 237 257 POTENTIAL.
CC DOMAIN 258 291 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 292 312 POTENTIAL.
CC DOMAIN 313 359 VACUOLAR (POTENTIAL).
CC TRANSSEM 183 192 5 x 2 AA APPROXIMATE REPEATS OF H-G.
CC SQ SEQUENCE 359 AA; 39276 MW; 256A30702D1D197 CRC64;

Query Match 34.2%; Score 747; DB 1; Length 359;
Best Local Similarity 42.0%; Pred. No. 5, 9e-51;
Matches 148; Conservative 78; Mismatches 108; Indels 18; Gaps 4;

QY 82 PLTNSQLSLKVDSCDNCCKOREI-----LKORVKARLITAAVLYLPMIGELVGGYLAN 136
DB PVNLPSVELAVQSNHCHAKQSGSHPNSEKQARAKLVASALCLVFMIGELIGSYLAQ 79
QY 137 SLAINTDALHMTTDSAIITTLALWLSKSPKTEFTGFPHLEVLASAMISVLYIIMG 196
DB 80 SLAINTDALHMTTDSAIITTLALWLSKSPKTEFTGFPHLEVLASAMISVLYIIMG 139
QY 197 FLTYEAVORTIHNRYEINGDIMLTAAGVAVNVIMGFLNOSGRHSHSHLSPNSPTR 256
DB 140 VLYLAVORLISDYIKGDMITLISGCAVAVNIMGLALHOSGSHSHSHEDS--- 196
QY 257 GSGCERNHODSLAVRAAFVHALGDLVQSVGLAAYITRPFEXKADPCTVYFSLV 316
DB 197 -----QQQONPSVAAAFIHVVGDLQSVGLVAAYITRPFEXKADPCTVYFSLV 249
QY 317 APTTFPIIMDIYVILIEGSPSHANDVYIEALMKIEDVYSVDLNIWLSKSKTAIYHI 376
DB 250 LGTTTLTILDLVILVIEGTPKGVDFTTVKNLLSLVDGEALHSLHIMLYAQAPLYSVHI 309
QY 377 QLISSGSKMEVQSKANHLINTEFGYACTIQLQSYROEVDRTGANCSSS 428
DB 310 ALAQNVDV--QAVLKVARDRLOQKTRFHTMTIQLISYSEDM-KSCQECQGS 358

RESULT 5
ZNT3_MOUSE STANDARD; PRT; 388 AA.
ID ZNT3_MOUSE

```

```

AC P97441; P97511;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Zinc transporter 3 (Znt-3).
GN SLC30A3 OR ZNT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=129; TISSUE=Brain;
RX MEDLINE=97121493; PubMed=8962159;
RA Palmiter R.D., Cole T.B., Quaife C.D., Findley S.D.;
RT "Znt-3, a putative transporter of zinc into synaptic vesicles.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14934-14939(1996).
CC -1- FUNCTION: Involved in accumulation of zinc in synaptic vesicles.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Localized in the
CC membrane of synaptic vesicles (Probable).
CC -1- TISSUE SPECIFICITY: Brain and testis. In the brain, most abundant
CC in hippocampus and cerebral cortex. In the testis, expression is
CC restricted to germ cells and is highest in pachytene spermatocytes
CC and round spermatids.
CC -1- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC transporters (CDF, TC 2.A.4). SLC30A subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U76007; AAB39733.1; -.
CC EMBL; U76009; AAB39733.1; ALT SEQ.
CC EMBL; U76008; AAB39733.1; JOINED.
CC MGI; MGI:1345280; SLC30a3.
CC InterPro; IPR002524; Cation_efflux.
CC Pfam; PF01545; Cation_efflux; 1.
CC TIGRFAMs; TIGR01297; CDF; 1.
CC Zinc transport; Transport; Transmembrane; Multigene family.
CC K01
CC DOMAIN 1 75 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 76 96 POTENTIAL.
CC DOMAIN 97 105 VACUOLAR (POTENTIAL).
CC TRANSSEM 106 126 POTENTIAL.
CC DOMAIN 127 145 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 146 166 POTENTIAL.
CC DOMAIN 167 177 VACUOLAR (POTENTIAL).
CC TRANSSEM 178 198 POTENTIAL.
CC DOMAIN 199 235 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 236 256 POTENTIAL.
CC DOMAIN 257 263 VACUOLAR (POTENTIAL).
CC TRANSSEM 264 284 POTENTIAL.
CC DOMAIN 285 388 CYTOPLASMIC (POTENTIAL).
CC SQ SEQUENCE 388 AA; 41824 MW; 3CDD0A37074EEF41 CRC64;

Query Match 29.4%; Score 642; DB 1; Length 388;
Best Local Similarity 35.0%; Pred. No. 1e-42;
Matches 144; Conservative 85; Mismatches 132; Indels 50; Gaps 9;

QY 27 SARDPSEADGEGISRFNKLRYVAVDGESEAPRPVNGAHTLQADDSDLLDDELPLTNS 86
DB 17 SARDPSAGS--GL-----RLKSLFTPESELPPEP----- 45
QY 87 QLSLKVDSCNCKQ--REILKORVKAR--LITAAVLYLPMIGELVGGYIANSIAM 141
DB 46 --KLEGVAFHCHCKDVPQSGLSPEVQARRQLYAAACACVIFMGGEVVGVAHSLAIM 103
QY 142 TDALHMTDLSAIIITTLALWLSKSPKTEFTGFPHLEVLASAMISVLYIIMGFLYE 201
DB 104 TDAHLHLDIGSLASLPSLIMSTRPATRTMTFGHRSSTLGAALSVSLSMIVTGLLYL 163

```



```

QY 202 AVORTIMNYEINGDIMLITAAVAVANVIMGFLNOSGHRSHSLPENSPTRSAGE 261
Db 164 AFLLHSDYHIEGAMLTASTAVCANLMAFVHLQTPHSHSGAEYAP-----LE 218
QY 262 RNHQ-----DSLAVRAAFVHALGDLVQSVGLIAAYIIRFKPEYKIADPICTYVFSLLVA 317
Db 219 EGHVYPMISLQNTSVRAAFVHLGDLVQSVGLIAAYIIRFKPEYKIADPICTYVFSLLVA 278
QY 318 FTTFRITMDYVITLIEGVPASHANDYIKEMAKMKIEDYVSVEDINWISLTSKSTAIYVHI 377
Db 279 GSTAPTRLDVILVMEGAPRVEPEVPADTLISVPGVRAHDLHMLTLTYHVASAHLA 338
QY 378 LIPSSSKWEVQSKANHLINTFGMYRCTIQLQSYQEVDRITCANQSSS 428
Db 339 I--DSTADPEAVILAEASRLYRFGSSCTLQVQYQPEMAQ-CLRCQES 386

```

RESULT 6
ZNT3 HUMAN STANDARD; PRT, 388 AA.

```

AC 099725:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Zinc transporter 3 (Znt-3).
GS SLC30A3 OR ZNT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Temporal cortex;
RX MEDLINE=97121493; PubMed=8962159;
RA Palmer R.D., Cole T.B., Quaife C.J., Findley S.D.;
RT "Znt-3, a putative transporter of zinc into synaptic vesicles.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14934-14939 (1996).
CC -1- FUNCTION: Involved in accumulation of zinc in synaptic vesicles
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Localized in the
CC membrane of synaptic vesicles (Probable).
CC -1- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC transporters (CDF, TC 2.A.4). SLC30A subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U76010; AAB39732.1;
DR Genbank: HGNC:11014; SLC30A3.
DR MIM: 602878;
DR GO: GO:0005768; C:cytosol; TAS.
DR GO: GO:0005887; C:integral to plasma membrane; TAS.
DR GO: GO:0005624; C:membrane fraction; TAS.
DR GO: GO:0008021; C:synaptic vesicle; TAS.
DR GO: GO:0015633; F:zinc porter activity; TAS.
DR GO: GO:0006810; P:transport; TAS.
DR InterPro: IPR02524; Cation efflux.
DR Pfam: PF01545; Cation efflux; 1.
DR TIGRfam: TIGR01297; CDF; 1.
KW Zinc transporter; Transport; Transmembrane; Multigene family.
FT DOMAIN 1 75
FT TRASNEM 76 96
FT DOMAIN 97 105
FT TRASNEM 106 126
FT DOMAIN 127 145
FT TRASNEM 146 166
FT DOMAIN 167 177
FT VACUOLAR (POTENTIAL).

```

```

FT TRASNEM 178 198
FT DOMAIN 199 235
FT TRASNEM 236 256
FT DOMAIN 257 264
FT TRASNEM 265 285
FT DOMAIN 286 388
SQ SEQUENCE 388 AA; 41944 MW; 74B8E24F17CF4740 CRC64;

Query Match
Best Local Similarity 37.2%; Pred. No. 1,1e-40;
Matches 130; Conservative 81; Mismatches 132; Indels 6; Gaps 4;

QY 79 QDLPLTNSQLSKVDSCNCSKREILKQRYAR--LITAAVLYLVMIGELVGGYIAN 136
Db 39 EPLPESSKVEWPFHGHCRDPLPPGLTPERLHARQLYACAVCFVMAEYVGGYIAH 98
QY 137 SLAINTDALLMTDLSAIIITLALMLSSKPTKFTFGPHLEYSAMISVLYIIMG 196
Db 99 SLAINTDALLMLADVSGMWSGLFSLMLSTRPATRMTGMRSETLGLASVSLMTWG 158
QY 197 FLUYAVORTIMNYEINGDIMLITAAVAVANVIMGFLNOSGHRSHSLPENSPTR 256
Db 159 ILVYLAFAVLLHSDYHIEGAMLTASTAVCANLMAFVHLQTPHSHSGAEYAPLE 218
QY 257 GSGCERNQODSLAFAAFVHALGDLVQSVGLIAAYIIRFKPEYKIADPICTYVFSLLV 316
Db 219 -BGPQPLPLQNTSVRAAFVHLGDLVQSVGLIAAYIIRFKPEYKIADPICTYVFSICA 277
QY 317 AFTFRITMDYVITLIEGVPASHANDYIKEMAKMKIEDYVSVEDINWISLTSKSTAIYVHI 376
Db 278 LGSTAPTRLDVILVMEGAPRVEPEVPADTLISVPGVRAHDLHMLTLTYHVASAHL 337
QY 377 QLPSSSKWEVQSKANHLINTFGMYRCTIQLQSYQEVDRITCANQ 425
Db 338 AI--DSTADPEAVILAEASRLYRFGSSCTLQVQYQPEMAQ-CLRCQ 383

```

RESULT 7

```

ZITB_ECOLI STANDARD; PRT, 313 AA.
ID ZITB_ECOLI
AC P75757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Zinc transporter zitB.
GN ZITB OR B0752.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=9746617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RL "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1234-1238 (1997).
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitegawa K., Makino K., Masuda S., Miki T., Mizubuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horikuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155 (1996).

```

```

RN [3]
RP CHARACTERIZATION.
RC STRAIN=K12 / M3110;
RX MEDLINE=21335524; PubMed=11443104;
RA Gress G., Fan B., Rosen B.P., Franke S., Nies D.H., Rensing C.,
RT "ZltB (Ypgr), a member of the cation diffusion facilitator family, is
RT an additional zinc transporter in Escherichia coli.",
RL J. Bacteriol. 183:4664-4667(2001).
CC -1- FUNCTION: Involved in zinc efflux across the cytoplasmic membrane,
CC thus reducing zinc accumulation in the cytoplasm and rendering
CC bacteria more resistant to zinc. It may contribute to zinc
CC homeostasis at low concentrations of zinc, whereas zntA is
CC required for growth at more toxic concentrations.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- INDUCTION: By zinc.
CC -1- MISCELLANEOUS: Appears to be selective for zinc, not conferring
CC resistance to cobalt nor cadmium.
CC -1- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC transporters (CDF, TC 2.A.4). SLC30A subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB000177; AAC73839.1; -.
DR EMBL; D90714; BA35414.1; -.
DR PIR; H64810; H64810.
DR Ecogene; EG13662; zltB.
DR HAMAP; MF_00552; -.
DR InterPro; IPR002524; Cation_efflux.
DR Pfam; PF01545; Cation_efflux; 1.
DR TIGRFAMs; TIGR01297; CDF, 1.
KM TRANSPORT, Zinc transport; Transmembrane; Complete proteome.
FT TRANSMEM 21
FT TRANSMEM 48
FT TRANSMEM 68
FT TRANSMEM 90
FT TRANSMEM 122
FT TRANSMEM 142
FT TRANSMEM 160
FT TRANSMEM 180
FT TRANSMEM 202
FT DOMAIN 240
FT DOMAIN 313
SQ SEQUENCE 313 AA; 34678 MW; 36740D67EABAC907 CRC64;
Query Match 17.7%; Score 386; DB 1; Length 313;
Best Local Similarity 31.6%; Pred. No. 7, 1e-23;
Matches 92; Conservative 71; Mismatches 94; Indels 34; Gaps 7;
QY 124 FMIGELVGYIANSLAIMDACHMLDLSAIIITLALMSKSPKRTFGPHLEVLUS 183
DB 31 FMLEVVGGFLSSGLADAGMLDTALPLALAAVOPSRPPIRTHTFGLRTTLTA 90
QY 184 AMISVLLVYILMGFLLYEAVQRTTHNYEINGDMLITRAVGVAVVWVINGFLNOSGHRH 243
DB 91 AFVNAIALVYITILLIWEALER-FRTPRVEGGMMVAIVAGLLNIIISFWL----- 142
QY 244 SHHSLSPLNSPTFGSGCERNHGD--SLAVRAAFVHALGDVQSVGLIAATITFKPEY 301
DB 143 -----HSGSEKNLVNRAAAHVLGDLIGSGVAIIAIIIM-TGW 182
QY 302 KIADPICTVYFSLVAFTFTIIMDTVYIILEGVSHLNVDIKALMK-IDEYVSVDL 360
DB 183 TPADPIILSLIVSLVRSAMRLKDSVNNLLGAPSLDIALKRMCKREIYEVANVHV 242
QY 361 NIMSLISGKSTALVHQLIPGSSKKEVQSKANHLILTFMWRCTIOQL 411
DB 243 HWV-MWGEKPVMTLHVQVIPPDH-DALIDQIOHYIMDHYOIEHATIQME 290

```

```

ID ZITB_ECO57 STANDARD; PRT; 311 AA.
AC 08XA00; 08X3F7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Zinc transporter zltB.
GN ZITB OR Z0922 OR ECG9780.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glaser J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RL "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Ikeda T., Takami H., Honda T., Sasaki A., Ogasawara N., Yasunaga T.,
RA Kikura S., Shiba T., Hattori M., Shimogawa H.;
RL "Complete genome sequence of enterohaemorrhagic Escherichia coli
RL O157:H7 and genomic comparison with a laboratory strain X-12."
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: Involved in zinc efflux across the cytoplasmic membrane,
CC thus reducing zinc accumulation in the cytoplasm and rendering
CC bacteria more resistant to zinc. It may contribute to zinc
CC homeostasis at low concentrations of zinc (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC transporters (CDF, TC 2.A.4). SLC30A subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB005253; AAG5081.1; -.
DR EMBL; AP002553; BAB34203.1; -.
DR PIR; D90726; D90726.
DR PIR; B85577; B85577.
DR HAMAP; MF_00552; -.
DR InterPro; IPR002524; Cation_efflux.
DR Pfam; PF01545; Cation_efflux; 1.
DR TIGRFAMs; TIGR01297; CDF, 1.
KM TRANSPORT, Zinc transport; Transmembrane; Complete proteome.
FT TRANSMEM 19
FT TRANSMEM 39
FT TRANSMEM 46
FT TRANSMEM 66
FT TRANSMEM 88
FT TRANSMEM 108
FT TRANSMEM 120
FT TRANSMEM 140
FT TRANSMEM 158
FT TRANSMEM 178
FT TRANSMEM 180
FT TRANSMEM 200
FT DOMAIN 238
FT DOMAIN 311
FT DOMAIN 311
SQ SEQUENCE 311 AA; 34468 MW; 2D0F139E0C537587 CRC64;
Query Match 17.6%; Score 385; DB 1; Length 311;
Best Local Similarity 31.3%; Pred. No. 8, 5e-23;
Matches 91; Conservative 72; Mismatches 94; Indels 34; Gaps 7;

```

```

QY 124 FMIGELGGYANSIAINTDALHMLTDLSSAIILTLALMLSSKSPKRTTFFGHRLEVL 183
DB 29 FMLVEVIGGSLGSLALADAGHMLTDTAALLFALLAVQFSRRPPTIRHTFGMLRUTLLA 88
QY 184 AMISVLLVILMGFLLYEAVQRTIHMNYEINGDIMLITAAVAVNVIMGFLNQSCHRR 243
DB 89 AFVNAIALVITILIVWEAIER-FRTPRPVEGGWMAIAVAGLANILSPWLL----- 140
QY 244 SHSHLSPNSPTRGSGCERNHGD--SLAVRAAFVHALGDLVOSVGLIAAYIRKPEY 301
DB 141 -----HGSBEKLNVRRAALHVLGDLGSGVGAIAALIIIW-TGW 180
QY 302 KIADPICTVYFSLVAFTRITWDTVIILEGVPSHLNVDYIKKALMK-IEDVYSVEDL 360
DB 181 TPADPILSLVLSLVLRSANLLKDSVNLLEGAPVSLDIAELKREKREIPEVRNVHV 240
QY 361 NIMSLTSGKSTAIVHILQIPGSSKWEVOSKANHLNLTFTFGYRCITQIQ 411
DB 241 HVM-MVGEKPVMTLHVQVIPPDDH--DALLDQIQVILMDHYQIEHAHQME 288

RESULT 9
ZITB_SALTY STANDARD; PRT; 312 AA.
AC Q8ZQT3;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Zinc transporter zitB.
GN ZITB OR STM0758.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lt2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT Lt2."
RL Nature 413:852-856(2001).
CC -!- FUNCTION: Involved in zinc efflux across the cytoplasmic membrane,
CC thus reducing zinc accumulation in the cytoplasm and rendering
CC bacteria more resistant to zinc. It may contribute to zinc
CC homeostasis at low concentrations of zinc (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC transporters (CDF, TC 2.A.4). SLC30A subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE008731; AAU19697.1; -.
CC STyGene; SG????; zitB.
CC HAMAP; MF_00552; -; 1.
CC InterPro; IPR002524; Cation_efflux.
CC Pfam; PF01545; Cation_efflux; 1.
CC TIGRfams; TIGR01297; CDF; 1.
CC Transport; Zinc transport; Transmembrane; Complete proteome.
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.

```

```

FT TRANSMEM 164 184 POTENTIAL.
FT DOMAIN 240 312 HIS-RICH.
SQ SEQUENCE 312 AA; 34461 MW; 2521FF85B2B7B3A6 CRC64;

Query Match 17.2%; Score 376; DB 1; Length 312;
Best Local Similarity 31.0%; Pred. No. 4.3e-22;
Matches 93; Conservative 77; Mismatches 100; Indels 30; Gaps 8;

QY 113 RLTIAAVLYLPMIGELVGGYANSIAINTDALHMLTDLSSAIILTLALMLSSKSPKRT 172
DB 20 RLLFAFIYTAGFMLEVVGGILSGSLADAGHMLTDAALLFALLAVQFSRRPPTIRH 79
QY 173 TFGFHRLEVLGAMISVLLVILMGFLLYEAVQRTIHMNYEINGDIMLITAAVAVNVIM 232
DB 80 TFGWLRLTLAFAVNAIALVITILIVWEAIER-FYTPRPVAGNLMVIAVAGLANLFA 138
QY 233 GELLNQSGHRHSHSLPSNSTRGSGCERNHGD--SLAVRAAFVHALGDLVOSVGLIAA 292
DB 139 FWILH-----RGSD-EKN-----LNVRRAALHVMGDLGSGVGAIAA 174
QY 293 YTIREFKPKYIADPICTVYFSLVAFTRITWDTVIILEGVPSHLNVDYIKKALMK-I 351
DB 175 LIIIW-TGWTADPILSLVLSLVLRSANLLKDSVNLLEGAPVSLDIALQRLHLSREI 233
QY 352 EDVYSVEDLNISLTSGKSTAIVHILQIPGSSKWEVOSKANHLNLTFTFGYRCITQIQ 411
DB 234 PEVRNVHVHVW-MVGEKPVMTLHAQVIPPDDH--DALLRIQDFLMHEYHIAHAHQME 290

RESULT 10
ZITB_SALTY STANDARD; PRT; 312 AA.
AC Q8Z8B6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc transporter zitB.
GN ZITB OR STY0799 OR T2120.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Churcher C., Mungall K.L., Brooks K., Chillingworth T., Connor P.,
RA Baker S., Basham D., Davis R.M., Dowd L., White N., Farrar J.,
RA Cronin A., Davis P., Davies R.M., Dwell L., Hien T.T., Holroyd S., Jagers K.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Moulé S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
CC [2]
CC SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Involved in zinc efflux across the cytoplasmic membrane,
CC thus reducing zinc accumulation in the cytoplasm and rendering
CC bacteria more resistant to zinc. It may contribute to zinc
CC homeostasis at low concentrations of zinc (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC transporters (CDF, TC 2.A.4). SLC30A subfamily.
CC -----

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL627268; CAD05215.1; -
DR EMBL; AE016841; AAC89737.1; -
DR HAMAP; MF 00552; -; 1.
DR InterPro; IPR002524; Cation efflux.
DR Pfam; PF01545; Cation efflux; 1.
DR TIGRFAMs; TIGR01297; CDF; 1.
KW Transport; Zinc transport; Transmembrane; Complete proteome.
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT DOMAIN 240 312 HIS-RICH.
SQ SEQUENCE 312 AA; 34531 MW; EA29EF94B3A18736 CRC64;

Query Match 17.0%; Score 372; DB 1; Length 312;
Best Local Similarity 30.7%; Pred. No. 8.8e-22;
Matches 92; Conservative 77; Mismatches 101; Indels 30; Gaps 8;

QY 113 RLTAVALLLFMELGVGGYANSIAIMTDALHMLTDLAISILTLALWLSKSTKRF 172
DB 20 RLPAFIVTAGFMLEVVGGILSGSLADAGHMLTDAALFALLVQVFSRPTVH 79

QY 173 TFGFHRLEVSAMTSLVLLVILMGFLYEAQVTHNMVINGIMLITAAVGVAVNVIM 232
DB TFGMLRLTLTAFAFNAIALVITLLIWEAIER-FYTPRPVAGNLMWVIAVAGLLANLEA 138

QY 233 GFLANQSGHRHSHSLPSNSPTFGSGCERNHGODSLAVRAAFVHALGDLVQSVGLIAA 292
DB 139 FWILH-----RGSD-EKN-----LNVRRAALHVGWDDLGSVGAIVAA 174

QY 293 YIIRFPEYKIADPICTYVFLSVAFTTFRRIIWDTVIILGVPSHLNVDIYKEALMK-I 351
DB 175 LLIIV-TGTPADPILSVLSVLRSARWLLKXSVNELLEGAPVSLDINALQHLRSRI 233

QY 352 EDVYSVEDLAIWSLTSCKSTAIVHQLIPGSSKWEVQSKANHLILNFGVMVRCIIQLQ 411
DB 234 PEVRNVHVVHVM-MVGKPVNTLHAQVIPPDDH--DALLERIQDFLMHEYHIAHATIQME 290

RESULT 11
ZITB YERPE STANDARD; PRT; 312 AA.
AC Q8ZGYG;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc transporter zitB.
GN ZITB OR YF01129 OR Y3050.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J.B., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.N., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;

```

```

RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
CC -!- FUNCTION: Involved in zinc efflux across the cytoplasmic membrane,
CC thus reducing zinc accumulation in the cytoplasm and rendering
CC bacteria more resistant to zinc. It may contribute to zinc
CC homeostasis at low concentrations of zinc (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -!- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC transporters (CDF, TC 2.A.4). SLC30A subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ414146; CAC89972.1; -
DR EMBL; AE013906; AAM86600.1; -
DR FIR; A0138; A0138.
DR HAMAP; MF 00552; -; 1.
DR InterPro; IPR002524; Cation efflux.
DR Pfam; PF01545; Cation efflux; 1.
DR TIGRFAMs; TIGR01297; CDF; 1.
KW Transport; Zinc transport; Transmembrane; Complete proteome.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 40 60 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT DOMAIN 235 312 HIS-RICH.
SQ SEQUENCE 312 AA; 34827 MW; B727B66194A66705 CRC64;

Query Match 16.3%; Score 355; DB 1; Length 312;
Best Local Similarity 27.5%; Pred. No. 1.9e-20;
Matches 85; Conservative 77; Mismatches 117; Indels 30; Gaps 6;

QY 104 ILKQKVKARLTIAAVLYLFLMIGELVGGYANSIAIMTDALHMLTDLAISILTLALWL 163
DB 6 IFSQDSNSKRLIIAFAITTLFWVTEAIGWLSGSLADAGHMLTDSALFIALMAVHF 65

QY 164 SSKPTKRFTEGPHRLEVSAMISVLLVYILMGFLYEAQVTHNMVINGIMLITAA 223
DB 66 SORXPDPRHTFGYLRLLTAAAFVNAALLVILVWEAVER-FPSPEVNGTPLLIIAI 124

QY 224 VGVAVNVMGFLNQSGHRHSHSLPSNSPTFGSGCERNHGODSLAVRAAFVHALGDLV 283
DB 125 AGLLANIFCFWILH-----KGEEKKNINVRRAALHVLSDLL 160

QY 284 QSVGVIAAYIIRFPEYKIADPICTYVFLSVAFTTFRRIIWDTVIILGVPSHLNVDIY 343
DB 161 GSVGAMIAAIVI-LTTGTPTDIPILSVLSVLRSARWLLKESFHELLEGAPQEIINK 219

QY 344 I-KEALMKIEDVYSVEDLNIWSLTSCKSTAIVHQLIPGSSKWEVQSKANHLILNFG 402
DB 220 LRKOLCTNIYEVRIHVVHLMQVGEQRLMTL-HAQVIPPDDH--DALLQRIQDYLLHYR 276

QY 403 MYRCITQLQ 411
DB 277 ISHATVQME 285

```

```

RESULT 12
ID  CZCD  ALCEU  STANDARD;  PRT;  316 AA.
AC  DT  01-JAN-1990 (Rel. 13, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Cobalt-zinc-cadmium resistance protein czcd (Cation efflux system
DE  protein czcd).
GN  CZCD.
OS  Alkaligenes eutrophus (Ralstonia eutropha).
OC  Plasmid pMOL30.
OC  Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC  Burkholderiaceae; Ralstonia.
OX  NCBI_TaxID=510;
RN  [1]
RP  PRELIMINARY SEQUENCE FROM N.A.
RC  STRAIN=CH34;
RX  MEDLINE=97197194; PubMed=9044283;
RA  van der Lelie D., Schwuchow T., Schwidetzky T., Wuerztz S.,
RA  Baeyens W., Mergey M., Nies D.H.;
RT  "Two-component regulatory system involved in transcriptional control
RT  of heavy-metal homeostasis in Alkaligenes eutrophus.";
RL  Mol. Microbiol. 23:493-503(1997).
CC  -!- FUNCTION: Necessary for activation of the czc determinant.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC  -!- INDUCTION: By zinc.
CC  -!- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC  transporters (CDF, TC 2.A.4). SUC30A subfamily.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; X98451; CAA67085.1; -.
DR  InterPro; IPR002524; Cation efflux.
DR  Pfam; PF01545; Cation_efflux; 1.
DR  TIGRFAMs; TIGR01297; CDF; 1.
KW  Transport; Zinc transport; Cadmium resistance; Cadmium; Cobalt;
KW  Transmembrane; Plasmid.
FT  TRANSMEM 17 37 POTENTIAL.
FT  TRANSMEM 47 67 POTENTIAL.
FT  TRANSMEM 82 102 POTENTIAL.
FT  TRANSMEM 115 135 POTENTIAL.
FT  TRANSMEM 152 172 POTENTIAL.
FT  TRANSMEM 174 194 POTENTIAL.
SQ  SEQUENCE 316 AA; 33707 MW; 2977C1B4AE9600F CRC64;

Query Match 16.2%; Score 353; DB 1; Length 316;
Best Local Similarity 30.8%; Pred. No. 2.7e-20;
Matches 92; Conservative 67; Mismatches 110; Indels 30; Gaps 6;

QY 114 LTIAAVLYLFLMIGELVGGYIANSIAIMTDALHMLTDLAISILTLALMLSSKSPKRT 173
DB 17 LKIALALTGTFLIAEVVGGVWTKSLATSDAAHMLTDTVALATAAIAIAKRPADKRT 76

QY 174 RGFHEVLISAMISVLVYILMGFLLYEAVQRTIHMNYEINGDIMLITRAAVGVAVNIMG 233
DB 77 FGYYRFEILAAAFNALLLFGVAIYLYEAYLR-LKSPQPIESTGMFVVAVLGLIINLISM 135

RESULT 13
ID  CZCD  ALCSP  STANDARD;  PRT;  316 AA.
AC  P94178;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Cation efflux system protein czcd.
GN  CZCD.
OS  Alkaligenes sp. (strain CT14).
OC  Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC  Alkaligenaceae; Alkaligenes.
OX  NCBI_TaxID=512;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96219090; PubMed=8829543;
RA  Kunito T., Kusano T., Oyaizu H., Senoo K., Kanazawa S.,
RA  Matsumoto S.;
RT  "Cloning and sequence analysis of czc genes in Alkaligenes sp. strain
RT  CT14.";
RL  Biosci. Biotechnol. Biochem. 60:699-704(1996).
CC  -!- FUNCTION: Necessary for activation of the czc determinant.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC  -!- SIMILARITY: Belongs to the cation diffusion facilitator family of
CC  transporters (CDF, TC 2.A.4). SLC30A subfamily.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; D67044; BAA11062.1; -.
DR  PIR; JC4701; JC4701.
DR  InterPro; IPR002524; Cation efflux.
DR  Pfam; PF01545; Cation_efflux; 1.
DR  TIGRFAMs; TIGR01297; CDF; 1.
KW  Transport; Transmembrane; Zinc transport; Cadmium; Cobalt.
KW  TRANSMEM 17 37 POTENTIAL.
FT  TRANSMEM 47 67 POTENTIAL.
FT  TRANSMEM 82 102 POTENTIAL.
FT  TRANSMEM 115 135 POTENTIAL.
FT  TRANSMEM 152 172 POTENTIAL.
FT  TRANSMEM 174 194 POTENTIAL.
SQ  SEQUENCE 316 AA; 33741 MW; D677C1B4A1E96462 CRC64;

Query Match 16.2%; Score 353; DB 1; Length 316;
Best Local Similarity 30.8%; Pred. No. 2.7e-20;
Matches 92; Conservative 67; Mismatches 110; Indels 30; Gaps 6;

QY 114 LTIAAVLYLFLMIGELVGGYIANSIAIMTDALHMLTDLAISILTLALMLSSKSPKRT 173
DB 17 LKIALALTGTFLIAEVVGGVWTKSLATSDAAHMLTDTVALATAAIAIAKRPADKRT 76

QY 174 RGFHEVLISAMISVLVYILMGFLLYEAVQRTIHMNYEINGDIMLITRAAVGVAVNIMG 233
DB 77 FGYYRFEILAAAFNALLLFGVAIYLYEAYLR-LKSPQPIESTGMFVVAVLGLIINLISM 135

```

QY 234 FLINQSGHSHSLSPNPTGSGCGRHGDLSLAVRAAFVHALGDLVQSVGLIAY 293
 DB 136 RMLS-SGO-----SSSLNVKGAYLEVSDLLSGVGIAGAI 170
 QY 294 IIRKPKYKIADPCTVYVSVLLVAFTRIIWDTVILLEGVPSHLNVDYIKALKMKIED 353
 DB 171 IIRP-TGMAWDSIAVLIGLWLPRTWFLKSLNVLGSDVDVLAVERKQLATPG 229
 QY 354 VYVEDLNINSLTSGKTAIVHQLIPGSSKWE-EVQSKANHLNLTNFGNYCTIQLQ 411
 DB 230 VKSPFDLHLWALTSGKSLTHV--VNDTAVNPEMEVLPELQMLADKFDITHVTIQFE 286

RESULT 14

COTL_YEAST
 ID COTL_YEAST STANDARD; PRT; 439 AA.
 AC P32798;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cobalt uptake protein COTL.
 GN COTL OR YOR316C OR Osl31.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]

RP SEQUENCE FROM N.A.
 RA MEDLINE=92375034; PubMed=1508175;
 RA Conklin D.S., McMaster J.A., Culbertson M.R., Kung C.;
 RA "COT1, a gene involved in cobalt accumulation in Saccharomycetes
 RT cerevisiae";
 RL Mol. Cell. Biol. 12:3678-3688(1992).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=5288c; / F1679;
 RA MEDLINE=97051589; PubMed=8896266;
 RA Pearson B.M., Hernandez Y., Payne J., Wolf S.S., Kalogeropoulos A.,
 RA Schweizer M.;
 RT "Sequencing of a 35.71 kb DNA segment on the right arm of yeast
 RT chromosome XV reveals regions of similarity to chromosomes I and
 RT XIII";
 RL Yeast 12:1021-1031(1996).

CC -!- FUNCTION: PROBABLY RESPONSIBLE FOR THE UPTAKE OF COBALT IONS. IT
 CC APPEARS TO ACT IN A DOSAGE-DEPENDENT MANNER TO COUNTERACT THE
 CC ADVERSE EFFECTS OF COBALT IONS ON CELLS. IT MAY PARTICIPATE IN
 CC THE REGULATION OF COBALT LEVELS UNDER NORMAL PHYSIOLOGICAL
 CC CONDITIONS AND MAY BE IMPORTANT IN THE SUPPLY OF METAL THAT IS
 CC REQUIRED FOR METALLOENZYME OR COPACITOR SYNTHESIS. IT REDUCES THE
 CC TOXICITY OF COBALT AND RHODIUM IONS. OTHER COMPONENTS RESPONSIBLE
 CC FOR COBALT TRANSPORT EXIST.

CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. ANOTHER POSSIBILITY
 CC EXISTS THAT IT IS ASSOCIATED WITH ANOTHER UNIDENTIFIED MEMBRANE
 CC THAT HAS BEEN ENRICHED IN THE MITOCHONDRIAL MEMBRANE FRACTIONS.

CC -!- SIMILARITY: Belongs to the cation diffusion facilitator family of
 CC transporters (CDF, TC 2.A.4). SLC30A subfamily.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; M88252; AAA74884.1; -;
 CC EMBL; X90565; CAA62171.1; -;
 CC EMBL; Z75224; CAA99636.1; -;
 CC PIR; S58327; S58327;
 CC GeneOnline; 143904; -;
 CC SGD; S0005843; COTL; -;
 CC GO; GO:0000324; C: vacuole (sensu Fungi); IDA.

DR GO; GO:0015087; P: cobalt ion transporter activity; IMP.
 DR GO; GO:0005385; P: zinc ion transporter activity; IGI.
 DR GO; GO:0006824; P: cobalt ion transport; IMP.
 DR GO; GO:0006829; P: zinc ion homeostasis; IMP.
 DR GO; GO:0006829; P: zinc ion transport; IGI.
 DR InterPro; IPR002524; Cation efflux.
 DR Pfam; PF01545; Cation efflux; 1.
 DR TIGRFam; TIGR01297; CDF; 1.
 KW Transport; Cobalt; Mitochondrion; Transmembrane.
 FT TRANSMEM 10 27 POTENTIAL.
 FT TRANSMEM 43 60 POTENTIAL.
 FT TRANSMEM 78 100 POTENTIAL.
 FT TRANSMEM 114 133 POTENTIAL.
 FT TRANSMEM 244 265 POTENTIAL.
 FT TRANSMEM 279 295 POTENTIAL.
 FT DOMAIN 140 148 HIS-RICH; COULD BE INVOLVED IN
 FT DOMAIN 163 169 COORDINATION OF COBALT IONS.
 FT CONFLICT 227 227 HIS-RICH; COULD BE INVOLVED IN
 FT CONFLICT 333 334 COORDINATION OF COBALT IONS.
 FT CONFLICT 424 424 G -> E (IN REF. 1).
 FT CONFLICT 424 424 HI -> RV (IN REF. 1).
 FT CONFLICT 424 424 I -> V (IN REF. 1).
 SQ SEQUENCE 439 AA; 48154 MW; AC88AAAF2EB4AD CRC64;

Query Match 15.7%; Score 343; DB 1; Length 439;
 Best Local Similarity 25.3%; Pred. No. 2.4e-13;
 Matches 101; Conservative 77; Mismatches 123; Indels 98; Gaps 12;

QY 106 KQKVKAEITIAAVLYLLFMIGELVGVGVIANSLAIMTDALHMLTDLSSAILTLALW--- 162
 DB 6 KQVLIISLLDTVFFGI---EITGVLSHSLADSFHMLND---IISLVVALWAVN 58
 QY 163 -LSKSPKTRFTFGHRLVLSAMISVLLVYLMGLLYEAVORTIHNNVEINGDIMLT 221
 DB 59 VAKRNPDSVTYGVKRAEILGALINAVFLIALCVSILIEALQRIAPPVIENPKFVLV 118
 QY 222 AAVGVANVIMGFLN---QSHRHSHS-----LPS----- 251
 DB 119 GVAGLISNTVGLFLFHDNDQHGHHGSHGGIFADHEMMMPSSHHTTHAHVDGIENTTP 178
 QY 252 -----NSPTR-----GSCERNHQDS 268
 DB 179 MDSTDNISEIMPNAIVDSFVNTRLTTPENASKTPSYSTSSHTIASGGNVTENKRS 238
 QY 269 LAVRAAFVHALGDLVQSVGLIAYIIRPKPEYK---IADPCTYVSLVAFTRIIW 325
 DB 239 LNMHGVLHLVGLDAGLGNIGVMSAFFI-WKTDYSWKYTPDPLVSLIITGIFFSALPLSC 297
 QY 326 DTWVILLEGVPSHLNVDYIKALKMKIEDVYVSDLNWISLTSGKSTAIHVHQLIPGSSSK 385
 DB 298 KASKILLQATSTLSGQDVEGDLKIPGIAIHDFHNLNLTESIFIASLHQL-DISPEQ 356
 QY 386 WEE-----VQSKANHLNLTNFGNYCTIQLQSYROEVDR 420
 DB 357 FTDLAKIVRSK-----LHRYGIHSATLQPEFITREVTST 390

RESULT 15

ZRC1_YEAST
 ID ZRC1_YEAST STANDARD; PRT; 442 AA.
 AC P20107;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc/cadmium resistance protein.
 GN ZRC1 OR YMR243C OR YMR408.05C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DKD-5D-H;


```

RX MEDLINE=90136503; PubMed=2693940;
RA Kaminishi A., Nishizawa M., Teramishi Y., Murata K., Kimura A.;
RT "Identification of a gene conferring resistance to zinc and cadmium
RL ions in the yeast Saccharomyces cerevisiae.";
RN Mol. Gen. Genet. 219:161-167(1989).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA MEDLINE=97313268; PubMed=9169872;
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels R., Lye G., Moule S., Odell C., Pearson D., Rajadream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII.";
RL Nature 387:90-93(1997).
RC CL - ION FUNCTION: Probably responsible for the uptake of zinc and cadmium
CC CC - ION SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC CC (Potential).
CC CC - ION SIMILARITY: Belongs to the cation diffusion facilitator family of
CC CC transporters (CDF, TC 2.A.4). SUC30A subfamily.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL; X17537; CAB56542.1; -.
CC DR EMBL; Z48756; CAA88653.1; -.
CC DR PIR; S56057; S56057.
CC DR Garmonline; 142918; -.
CC DR SGD; S0004856; ZRC1.
CC DR GO; GO:0000324; C:Vacuole (sensu Fungi); IDA.
CC DR GO; GO:0005385; F:zinc ion transporter activity; IMP.
CC DR GO; GO:0006824; P:cobalt ion transport; NAS.
CC DR GO; GO:0006749; P:glutathione metabolism; NAS.
CC DR GO; GO:0006882; P:zinc ion homeostasis; IMP.
CC DR GO; GO:0006829; P:zinc ion transport; NAS.
CC DR InterPro; IPR002524; Cation_efflux.
CC DR Pfam; PF01545; Cation_efflux; 1.
CC DR TIGRFAMs; TIGR01297; CDF; 1.
CC DR Transmembrane; Zinc transport; Cadmium resistance; Mitochondrion; Cadmium;
KW KW Transmembrane; Glycoprotein.
FT FT TRANSMEM 10 26 POTENTIAL.
FT FT TRANSMEM 42 58 POTENTIAL.
FT FT TRANSMEM 80 96 POTENTIAL.
FT FT TRANSMEM 113 129 POTENTIAL.
FT FT TRANSMEM 240 256 POTENTIAL.
FT FT TRANSMEM 270 286 POTENTIAL.
FT FT DOMAIN 141 145 HIS-RICH; COULD BE INVOLVED IN
FT FT DOMAIN 163 167 COORDINATION OF ZINC OR CADMIUM IONS.
FT FT DOMAIN 216 220 HIS-RICH; COULD BE INVOLVED IN
FT FT DOMAIN 414 414 COORDINATION OF ZINC OR CADMIUM IONS.
FT FT CONFLICT 417 417 HIS-RICH; COULD BE INVOLVED IN
FT FT CONFLICT 417 417 COORDINATION OF ZINC OR CADMIUM IONS.
FT FT CONFLICT 417 417 R -> S (IN REF. 1).
FT FT CONFLICT 417 417 T -> I (IN REF. 1).
SQ SEQUENCE 442 AA; 48344 MW; CBE6AA9716C0CEBE CRC64;

Query Match 15.7%; Score 342; DB 1; Length 442;
Best Local Similarity 26.1%; Pred. No. 2.9e-19;
Matches 98; Conservative 73; Mismatches 123; Indels 82; Gaps 12;

QY 106 KQKVKARLTAAVLYLFLFMIGELVGGVIANSLMTDALHMLTDLSSAILTLALW--- 162
Db 5 KEKRIISLLDVTNFFFL---ETIYGNSHSLATADSFHMLND---IISLLVALNWD 57
QY 163 -LSKSPKTRFTFGFHRLEVLSAMSVLLVYILMGFLLYFAVORTIHMNYEINGDMLIT 221

```

Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 17:43:15 ; Search time 46 Seconds
(without alignments)
2925.434 Million cell updates/sec

Title: US-10-024-652-2570

Perfect score: 2183

Sequence: 1 MAGSGAWKRLKSLMRKDDAP.....LQSYRQEVDRTCANQCSSSP 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 segs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2183	100.0	429	15	US-10-024-652-2570 Sequence 2570, Ap
2	2183	100.0	429	15	US-10-024-652-2572 Sequence 2572, Ap
3	2183	100.0	429	15	US-10-024-652-2575 Sequence 2575, Ap
4	2183	100.0	429	15	US-10-024-652-2576 Sequence 2576, Ap
5	2183	100.0	429	15	US-10-024-652-2577 Sequence 2577, Ap
6	2183	100.0	429	15	US-10-024-652-2578 Sequence 2578, Ap
7	2183	100.0	429	15	US-10-295-027-544 Sequence 544, App
8	2183	100.0	438	10	US-09-357-708-27 Sequence 27, Appl
9	2179	99.8	429	14	US-10-345-680-53 Sequence 53, Appl
10	2179	99.8	429	15	US-10-024-652-2574 Sequence 2574, Ap
11	2179	99.8	429	15	US-10-024-652-2579 Sequence 2579, Ap
12	2176	99.7	428	15	US-10-024-652-2580 Sequence 2580, Ap
13	2166.5	99.2	430	15	US-10-012-697-1545 Sequence 1545, Ap
14	1990.5	91.2	429	15	US-10-024-652-2581 Sequence 2581, Ap
15	747	34.2	359	10	US-09-954-342-37 Sequence 37, Appl

Sequence 4, Appli
Sequence 4, Appli
Sequence 40, Appl
Sequence 40, Appl
Sequence 6, Appli
Sequence 8, Appli
Sequence 12, Appl
Sequence 22, Appl
Sequence 20, Appl
Sequence 38, Appl
Sequence 10, Appl
Sequence 39, Appl
Sequence 44, Appl
Sequence 52, Appl
Sequence 200, App
Sequence 60835, A
Sequence 61150, A
Sequence 111869, A
Sequence 3313, Ap
Sequence 221580, A
Sequence 50591, A
Sequence 42, Appl
Sequence 51, Appl
Sequence 57, Appl
Sequence 42, Appl
Sequence 221581, A
Sequence 58, Appl
Sequence 185725, A
Sequence 14576, A
Sequence 4910, Ap

US-10-114-270-4
US-10-380-727-4
US-10-162-012-40
US-10-162-102-40
US-10-114-270-6
US-09-554-342-8
US-09-954-342-12
US-09-872-153-22
US-10-176-306-20
US-09-954-342-38
US-09-954-342-10
US-09-954-342-39
US-10-369-022-44
US-10-176-306-52
US-09-826-734-200
US-10-425-114-60835
US-10-425-114-61150
US-10-437-963-111869
US-10-104-047-3913
US-10-424-599-221580
US-10-425-114-50591
US-10-162-012-42
US-10-176-306-51
US-10-176-306-57
US-10-162-102-42
US-10-424-599-221581
US-10-176-306-58
US-10-424-599-185725
US-10-156-761-14576
US-09-738-626-4910

ALIGNMENTS

RESULT 1

US-10-024-652-2570
Sequence 2570, Application US/10024652
Publication No. US20030219738A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E.H.
APPLICANT: Hubert, Rene S.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Levin, Elana
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108PSH8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REFERENCE: 51158-20025.00
CURRENT APPLICATION NUMBER: US/10/024,652
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2570
LENGTH: 429
TYPE: PRT
ORGANISM: homo sapien
US-10-024-652-2570

Query Match 100.0%; Score 2183; DB 15; Length 429;

Best Local Similarity 100.0%; Pred. No. 3.3e-218;

Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSGAWKRLKSLMRKDDAPFLNDSAFDFSDGDEGLSRFNKLRVVVADGSEAPER 60

Db 1 MAGSGAWKRLKSLMRKDDAPFLNDSAFDFSDGDEGLSRFNKLRVVVADGSEAPER 60

```
QY 61 PVNGAHTLQADDSSLLDQDLPLTNSQLSLKVDSCDNCQKREILKQKVKARLTIAAVL 120
DB 61 PVNGAHTLQADDSSLLDQDLPLTNSQLSLKVDSCDNCQKREILKQKVKARLTIAAVL 120
QY 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALLWLSSKSPTRKFTFGPHRLE 180
DB 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALLWLSSKSPTRKFTFGPHRLE 180
QY 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
DB 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
QY 241 HRHSHSLPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAIIIRFKPE 300
DB 241 HRHSHSLPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAIIIRFKPE 300
QY 301 YKIADPCTVYFSLVAFVFTFRIIWDTVIILGVPVSHLVNDYIKEALMKIEDVYSVEDL 360
DB 301 YKIADPCTVYFSLVAFVFTFRIIWDTVIILGVPVSHLVNDYIKEALMKIEDVYSVEDL 360
QY 361 NIWSLTSGKSTAVIHQILPGSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
DB 361 NIWSLTSGKSTAVIHQILPGSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
QY 421 CANCQSSSP 429
DB 421 CANCQSSSP 429
```

RESULT 2

```
US-10-024-652-2572
; Sequence 2572, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Eliana
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024,652
; PRIOR FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2572
; LENGTH: 429
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-2572
```

```
Query Match 100.0%; Score 2183; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 3.3e-218;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAGGAWKRLKSLRKDDAPFLNDTSAPDFSDEAGDEGLSRFNKLRVVVADGSEAPER 60
DB 1 MAGGAWKRLKSLRKDDAPFLNDTSAPDFSDEAGDEGLSRFNKLRVVVADGSEAPER 60
QY 61 PVNGAHTLQADDSSLLDQDLPLTNSQLSLKVDSCDNCQKREILKQKVKARLTIAAVL 120
DB 61 PVNGAHTLQADDSSLLDQDLPLTNSQLSLKVDSCDNCQKREILKQKVKARLTIAAVL 120
```

```
QY 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALLWLSSKSPTRKFTFGPHRLE 180
DB 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALLWLSSKSPTRKFTFGPHRLE 180
QY 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
DB 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
QY 241 HRHSHSLPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAIIIRFKPE 300
DB 241 HRHSHSLPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAIIIRFKPE 300
QY 301 YKIADPCTVYFSLVAFVFTFRIIWDTVIILGVPVSHLVNDYIKEALMKIEDVYSVEDL 360
DB 301 YKIADPCTVYFSLVAFVFTFRIIWDTVIILGVPVSHLVNDYIKEALMKIEDVYSVEDL 360
QY 361 NIWSLTSGKSTAVIHQILPGSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
DB 361 NIWSLTSGKSTAVIHQILPGSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
QY 421 CANCQSSSP 429
DB 421 CANCQSSSP 429
```

RESULT 3

```
US-10-024-652-2575
; Sequence 2575, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Eliana
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024,652
; PRIOR FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2575
; LENGTH: 429
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-2575
```

```
Query Match 100.0%; Score 2183; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 3.3e-218;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAGGAWKRLKSLRKDDAPFLNDTSAPDFSDEAGDEGLSRFNKLRVVVADGSEAPER 60
DB 1 MAGGAWKRLKSLRKDDAPFLNDTSAPDFSDEAGDEGLSRFNKLRVVVADGSEAPER 60
QY 61 PVNGAHTLQADDSSLLDQDLPLTNSQLSLKVDSCDNCQKREILKQKVKARLTIAAVL 120
DB 61 PVNGAHTLQADDSSLLDQDLPLTNSQLSLKVDSCDNCQKREILKQKVKARLTIAAVL 120
QY 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALLWLSSKSPTRKFTFGPHRLE 180
DB 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALLWLSSKSPTRKFTFGPHRLE 180
QY 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
```

Db	181	VLSAMLSVLLVTLKGFLLYEAQVTHHNYEINGDLMILTAAGVANVMIFGLNQSG	240
Qy	241	HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAYIIIRFKE	300
Db	241	HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAYIIIRFKE	300
Qy	301	YKIADPICYVYFSLVAVTTFRRIWDTVVILLEGVPSHLNDYIKALMKIEDVSVEDL	360
Db	301	YKIADPICYVYFSLVAVTTFRRIWDTVVILLEGVPSHLNDYIKALMKIEDVSVEDL	360
Qy	361	NIWSLTSGKSTAIHVHQLIPGSSSKWEEVQSKANHELLNTFGMYRCTIQLQSYRQEVDR	420
Db	361	NIWSLTSGKSTAIHVHQLIPGSSSKWEEVQSKANHELLNTFGMYRCTIQLQSYRQEVDR	420
Qy	421	CANCQSSSP	429
Db	421	CANCQSSSP	429

RESULT 4
US-10-024-652-2576
; Sequence 2576, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Elana
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; TITLE OF INVENTION: Detection of Cancer
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024,652
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/2556,210
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2576
; LENGTH: 429
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-2576

```

Db      241  HRHSHSLPSNSTRGCGCERNHGQDQLAVRAAFVHALGDLVOSGVLI AAYIIRFKPE 300
Qy      301  YKIADPCTCTVFSLLVAFTFRRIIWDTVWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
Db      301  YKIADPCTCTVFSLLVAFTFRRIIWDTVWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
Qy      361  NIWSLTGSKTAIVHIIQLIPGSSSKWEVOSKANHLIINTFGMYRCTIQLQSYRQEVDR 420
Db      361  NIWSLTGSKTAIVHIIQLIPGSSSKWEVOSKANHLIINTFGMYRCTIQLQSYRQEVDR 420
Qy      421  CANCQSSSP 429
Db      421  CANCQSSSP 429

RESULT 5
US-10-024-652-2577
; Sequence 2577, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Eliana
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; TITLE OF INVENTION: Detection of Cancer
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024,652
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,210
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2577
; LENGTH: 429
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-2577

```

```

; SEQ ID NO 4296
; LENGTH: 429
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-2576

Query Match          100.0%; Score 2183; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 3.3e-218;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1  MAGSGAWKELKSLMRKDDAPLNDTSAPFSDSDBAGDEGLSRFNKLRVVVVADGCSAPER 60
      |||
Db       1  MAGSGAWKELKSLMRKDDAPLNDTSAPFSDSDBAGDEGLSRFNKLRVVVVADGCSAPER 60
      |||

QY      61  PVNGAHTTLOADDSSLDDPLNTSQLSKVDSCDNCQREILKQRYKARLTIAAVL 120
      |||
Db       61  PVNGAHTTLOADDSSLDDPLNTSQLSKVDSCDNCQREILKQRYKARLTIAAVL 120
      |||

QY      121  YLLFMWIGELVGGYIANSIAIMTDALHMLTDLSAILLTLLALWSSKSPTKRPTFGFHRLE 180
      |||
Db       121  YLLFMWIGELVGGYIANSIAIMTDALHMLTDLSAILLTLLALWSSKSPTKRPTFGFHRLE 180
      |||

QY      181  VLSAMISVLVVLVILMGFLLYEAVQRTIEMNYEINGDMLTAAVGVAVNVIMGFILNQSG 240
      |||
Db       181  VLSAMISVLVVLVILMGFLLYEAVQRTIEMNYEINGDMLTAAVGVAVNVIMGFILNQSG 240
      |||

QY      241  HRHSHSHSLPNSPTRGSGCERNHQDGLAVRAAFVHALGDLVQSGVLIAAVIIRFKPE 300

```

Query Match	100.0%	Score 2183	DB 15	Length 429
Best Local Similarity	100.0%	Pred. No. 3.3e-218		
Matches 429	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MAGSGAWKRLKMLKDDAPLFLNDTSAFDFSDSAGDEGLSRFNKLRVVVADGSEAPER	60	
Db	1	MAGSGAWKRLKMLKDDAPLFLNDTSAFDFSDSAGDEGLSRFNKLRVVVADGSEAPER	60	
QY	61	PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCCKOREILKQKVKARUTIAAVL	120	
Db	61	PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCCKOREILKQKVKARUTIAAVL	120	
QY	121	YLLFMIGELVGGYIANSIAIMTDALHMLTDLSAILITLLALWLSSKSGPTKRTFGFHLE	180	
Db	121	YLLFMIGELVGGYIANSIAIMTDALHMLTDLSAILITLLALWLSSKSGPTKRTFGFHLE	180	
QY	181	VLSAMISVLLAVYILMGFLLYEAVQRTTHMNEYINGDILMTAAAVGVAVNVIMGFLINQSG	240	
Db	181	VLSAMISVLLAVYILMGFLLYEAVQRTTHMNEYINGDILMTAAAVGVAVNVIMGFLINQSG	240	
QY	241	HRSHSHSLSPNSPTRSGGCGERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAAYIIRKPE	300	
Db	241	HRSHSHSLSPNSPTRSGGCGERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAAYIIRKPE	300	
QY	301	YKIADPCTVVSLLVAFTTFRITWDTWVILGVPSPHLNVNDYIKEALMKTIEDVYSVDL	360	
Db	301	YKIADPCTVVSLLVAFTTFRITWDTWVILGVPSPHLNVNDYIKEALMKTIEDVYSVDL	360	

QY 361 NINSLTSGKSTAIWHIOLIFGSSSKWEVOSKANHLLNTFGMYRCTIOLOSQRQVDRT 420
 Db |||||

QY 421 CANCQSSSP 429
 Db |||||

RESULT 6
 US-10-024-652-2578
 ; Sequence 2578, Application US/10024652
 ; Publication No. US20030219738A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc
 ; APPLICANT: Challita-Eid, Pia M.
 ; APPLICANT: Faris, Mary
 ; APPLICANT: Afar, Daniel E.H.
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Mitchell, Steve Chappell
 ; APPLICANT: Levin, Eiana
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
 ; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
 ; TITLE OF INVENTION: Detection of Cancer
 ; FILE REFERENCE: 51158-20025.00
 ; CURRENT APPLICATION NUMBER: US/10/024,652
 ; CURRENT FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: 60/256,210
 ; PRIOR FILING DATE: 2000-12-15
 ; NUMBER OF SEQ ID NOS: 2598
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2578
 ; LENGTH: 429
 ; TYPE: PRT
 ; ORGANISM: homo sapien
 ; US-10-024-652-2578

Query Match 100.0%; Score 2183; DB 15; Length 429;
 Best Local Similarity 100.0%; Pred. No. 3.3e-218;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSGAWKRLKSMURKDDAPLNDTSAPFDSDEAGDEGLSRFNKLRVVVADGSEAPER 60
 Db |||||

QY 61 PVNGAHTLQADDDSLDDQDLPLTNSQLSKVSDCNCCKOREILKORKVKAULTIAAVL 120
 Db |||||

QY 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLISAIITLLALWSSKSPKRTFTGFPHRLE 180
 Db |||||

QY 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDMLITAAVGVAVNVINGFLNQS 240
 Db |||||

QY 241 HRHSHSLSPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAIIIFKPE 300
 Db |||||

QY 301 YKIADPCTIVFSLVLAFTFRITWDVTWVILEGVPSHLVNDVIKEALMKIEDVYVEDL 360
 Db |||||

QY 361 NINSLTSGKSTAIWHIOLIFGSSSKWEVOSKANHLLNTFGMYRCTIOLOSQRQVDRT 420
 Db |||||

QY 421 CANCQSSSP 429
 Db |||||

RESULT 7
 US-10-295-027-544
 ; Sequence 544, Application US/10295027
 ; Publication No. US20030232350A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsberg, Wendy M.
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Hevezi, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 ; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 ; FILE REFERENCE: 018501-012500US
 ; CURRENT APPLICATION NUMBER: US/10/295,027
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: US 09/663,733
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: US 60/350,666
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/335,394
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: US 60/332,464
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: US 60/334,393
 ; PRIOR FILING DATE: 2001-11-29
 ; PRIOR APPLICATION NUMBER: US 60/340,376
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: US 60/347,211
 ; PRIOR FILING DATE: 2002-01-08
 ; PRIOR APPLICATION NUMBER: US 60/347,349
 ; PRIOR FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 60/355,250
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 544
 ; LENGTH: 429
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-295-027-544

Query Match 100.0%; Score 2183; DB 15; Length 429;
 Best Local Similarity 100.0%; Pred. No. 3.3e-218;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSGAWKRLKSMURKDDAPLNDTSAPFDSDEAGDEGLSRFNKLRVVVADGSEAPER 60
 Db |||||

QY 61 PVNGAHTLQADDDSLDDQDLPLTNSQLSKVSDCNCCKOREILKORKVKAULTIAAVL 120
 Db |||||

QY 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLISAIITLLALWSSKSPKRTFTGFPHRLE 180
 Db |||||

QY 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDMLITAAVGVAVNVINGFLNQS 240
 Db |||||


```
Qy 241 HHHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGLIAAIIIRFKPE 300
Db 241 HHHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGLIAAIIIRFKPE 300
Qy 301 YKIADPCTVYVSLVAFTRIIIDWTWVILLEGVPSHLNVDYIKKALMKIEDVYSVEDL 360
Db 301 YKIADPCTVYVSLVAFTRIIIDWTWVILLEGVPSHLNVDYIKKALMKIEDVYSVEDL 360
Qy 361 NIMSLTSGKSTAIWHIOLIPGSSSKWEVQSKANHLILNTFGMYRCTIQLQSYRQEVDR 420
Db 361 NIMSLTSGKSTAIWHIOLIPGSSSKWEVQSKANHLILNTFGMYRCTIQLQSYRQEVDR 420
Qy 421 CANCQSSSP 429
Db 421 CANCQSSSP 429

RESULT 8
US-09-957-708-27
; Sequence 27, Application US/09957708
; Publication No. US20030031678A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Hervé
; APPLICANT: Caferkey, Robert
; APPLICANT: Ali, Shujath
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific
; TITLE OF INVENTION: Genes
; FILE REFERENCE: DEX-0239
; CURRENT APPLICATION NUMBER: US/09/957,708
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,746
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-708-27

Query Match 100.0%; Score 2183; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 3.4e-218;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAPFDSDEAGDEGLSRFNKLRVWVADDGSEAPER 60
Db 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAPFDSDEAGDEGLSRFNKLRVWVADDGSEAPER 60
Qy 61 PVNGAHTLOADDSDLLDQDPLPTNSQLSLKVDSCNCSKQREILKQKVKARLTIAAVL 120
Db 61 PVNGAHTLOADDSDLLDQDPLPTNSQLSLKVDSCNCSKQREILKQKVKARLTIAAVL 120
Qy 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISILTLALWLSKSPKFTFGFHRLE 180
Db 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISILTLALWLSKSPKFTFGFHRLE 180
Qy 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVANVINGFLNQSG 240
Db 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVANVINGFLNQSG 240
Qy 241 HHHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGLIAAIIIRFKPE 300
Db 241 HHHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGLIAAIIIRFKPE 300
Qy 301 YKIADPCTVYVSLVAFTRIIIDWTWVILLEGVPSHLNVDYIKKALMKIEDVYSVEDL 360
Db 301 YKIADPCTVYVSLVAFTRIIIDWTWVILLEGVPSHLNVDYIKKALMKIEDVYSVEDL 360
Qy 361 NIMSLTSGKSTAIWHIOLIPGSSSKWEVQSKANHLILNTFGMYRCTIQLQSYRQEVDR 420
Db 361 NIMSLTSGKSTAIWHIOLIPGSSSKWEVQSKANHLILNTFGMYRCTIQLQSYRQEVDR 420
```

```
Qy 421 CANCQSSSP 429
Db 421 CANCQSSSP 429

RESULT 9
US-10-345-680-53
; Sequence 53, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-345-680-53

Query Match 99.8%; Score 2179; DB 14; Length 429;
Best Local Similarity 99.8%; Pred. No. 8.7e-218;
Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAPFDSDEAGDEGLSRFNKLRVWVADDGSEAPER 60
Db 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAPFDSDEAGDEGLSRFNKLRVWVADDGSEAPER 60
Qy 61 PVNGAHTLOADDSDLLDQDPLPTNSQLSLKVDSCNCSKQREILKQKVKARLTIAAVL 120
Db 61 PVNGAHTLOADDSDLLDQDPLPTNSQLSLKVDSCNCSKQREILKQKVKARLTIAAVL 120
Qy 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISILTLALWLSKSPKFTFGFHRLE 180
Db 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISILTLALWLSKSPKFTFGFHRLE 180
Qy 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVANVINGFLNQSG 240
Db 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVANVINGFLNQSG 240
Qy 241 HHHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGLIAAIIIRFKPE 300
Db 241 HHHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGLIAAIIIRFKPE 300
Qy 301 YKIADPCTVYVSLVAFTRIIIDWTWVILLEGVPSHLNVDYIKKALMKIEDVYSVEDL 360
Db 301 YKIADPCTVYVSLVAFTRIIIDWTWVILLEGVPSHLNVDYIKKALMKIEDVYSVEDL 360
```

Db 301 YKIADPCTVYVSLVLAFTTFRITWDTVILGVPSHLVNDYIKEALMKIEDVYSVEDL 360

Qy 361 NIWLSLTSKSTAIYVHIQIIPGSSKWEVQSKANHLINTFGMYRCTIQLQSYRQEVDR 420

Db 361 NIWLSLTSKSTAIYVHIQIIPGSSKWEVQSKANHLINTFGMYRCTIQLQSYRQEVDR 420

Qy 421 CANCOSSSP 429

Db 421 CANCOSSSP 429

RESULT 10

US-10-024-652-2574

; Sequence 2574, Application US/10024652

; Publication No. US20030219738A1

; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc

; APPLICANT: Challita-Bid, Pia M.

; APPLICANT: Fafis, Mary

; APPLICANT: Afar, Daniel E.H.

; APPLICANT: Hubert, Rene S.

; APPLICANT: Mitchell, Steve Chappell

; APPLICANT: Levin, Elana

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc

; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and

; TITLE OF INVENTION: Detection of Cancer

; FILE REFERENCE: 51158-20025.00

; CURRENT APPLICATION NUMBER: US/10/024,652

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: 60/256,210

; PRIOR FILING DATE: 2000-12-15

; NUMBER OF SEQ ID NOS: 2598

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2574

; LENGTH: 429

; TYPE: PRT

; ORGANISM: homo sapien

US-10-024-652-2574

Query Match 99.8%; Score 2179; DB 15; Length 429;

Best Local Similarity 99.8%; Pred. No. 8.7e-218;

Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGSGAWKRLKSMURKDDAPLFLNDTSAPFSDSDEAGDEGLSRFNKLRVWVADDSSEAPER 60

Db 1 MAGSGAWKRLKSMURKDDAPLFLNDTSAPFSDSDEAGDEGLSRFNKLRVWVADDSSEAPER 60

Qy 61 PVNGAHTPLQADDDSLDDQDLPLTNSQLSKVDSKQREILKQKVKARLTIAAVL 120

Db 61 PVNGAHTPLQADDDSLDDQDLPLTNSQLSKVDSKQREILKQKVKARLTIAAVL 120

Qy 121 YLLFMIGELVGGYIANSIAINTDALHMLTDLTSAIILTLALWLSKSPKTRFTFGPHRLE 180

Db 121 YLLFMIGELVGGYIANSIAINTDALHMLTDLTSAIILTLALWLSKSPKTRFTFGPHRLE 180

Qy 181 VLSAMISVLLVYILMGFLLYEAQVQTHMNYEINGDMLITAAGVAVNVIMGFLNQSG 240

Db 181 VLSAMISVLLVYILMGFLLYEAQVQTHMNYEINGDMLITAAGVAVNVIMGFLNQSG 240

Qy 241 HRHSHSLPNSPTRSGGCGERNHGQDSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300

Db 241 HRHSHSLPNSPTRSGGCGERNHGQDSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300

Qy 301 YKIADPCTVYVSLVLAFTTFRITWDTVILGVPSHLVNDYIKEALMKIEDVYSVEDL 360

Db 301 YKIADPCTVYVSLVLAFTTFRITWDTVILGVPSHLVNDYIKEALMKIEDVYSVEDL 360

Qy 361 NIWLSLTSKSTAIYVHIQIIPGSSKWEVQSKANHLINTFGMYRCTIQLQSYRQEVDR 420

Db 361 NIWLSLTSKSTAIYVHIQIIPGSSKWEVQSKANHLINTFGMYRCTIQLQSYRQEVDR 420

Qy 421 CANCOSSSP 429

Db 421 CANCOSSSP 429

RESULT 11

US-10-024-652-2579

; Sequence 2579, Application US/10024652

; Publication No. US20030219738A1

; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc

; APPLICANT: Challita-Bid, Pia M.

; APPLICANT: Fafis, Mary

; APPLICANT: Afar, Daniel E.H.

; APPLICANT: Hubert, Rene S.

; APPLICANT: Mitchell, Steve Chappell

; APPLICANT: Levin, Elana

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc

; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and

; TITLE OF INVENTION: Detection of Cancer

; FILE REFERENCE: 51158-20025.00

; CURRENT APPLICATION NUMBER: US/10/024,652

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: 60/256,210

; PRIOR FILING DATE: 2000-12-15

; NUMBER OF SEQ ID NOS: 2598

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2579

; LENGTH: 429

; TYPE: PRT

; ORGANISM: homo sapien

US-10-024-652-2579

Query Match 99.8%; Score 2179; DB 15; Length 429;

Best Local Similarity 99.8%; Pred. No. 8.7e-218;

Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGSGAWKRLKSMURKDDAPLFLNDTSAPFSDSDEAGDEGLSRFNKLRVWVADDSSEAPER 60

Db 1 MAGSGAWKRLKSMURKDDAPLFLNDTSAPFSDSDEAGDEGLSRFNKLRVWVADDSSEAPER 60

Qy 61 PVNGAHTPLQADDDSLDDQDLPLTNSQLSKVDSKQREILKQKVKARLTIAAVL 120

Db 61 PVNGAHTPLQADDDSLDDQDLPLTNSQLSKVDSKQREILKQKVKARLTIAAVL 120

Qy 121 YLLFMIGELVGGYIANSIAINTDALHMLTDLTSAIILTLALWLSKSPKTRFTFGPHRLE 180

Db 121 YLLFMIGELVGGYIANSIAINTDALHMLTDLTSAIILTLALWLSKSPKTRFTFGPHRLE 180

Qy 181 VLSAMISVLLVYILMGFLLYEAQVQTHMNYEINGDMLITAAGVAVNVIMGFLNQSG 240

Db 181 VLSAMISVLLVYILMGFLLYEAQVQTHMNYEINGDMLITAAGVAVNVIMGFLNQSG 240

Qy 241 HRHSHSLPNSPTRSGGCGERNHGQDSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300

Db 241 HRHSHSLPNSPTRSGGCGERNHGQDSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300

Qy 301 YKIADPCTVYVSLVLAFTTFRITWDTVILGVPSHLVNDYIKEALMKIEDVYSVEDL 360

Db 301 YKIADPCTVYVSLVLAFTTFRITWDTVILGVPSHLVNDYIKEALMKIEDVYSVEDL 360

Qy 361 NIWLSLTSKSTAIYVHIQIIPGSSKWEVQSKANHLINTFGMYRCTIQLQSYRQEVDR 420

Db 361 NIWLSLTSKSTAIYVHIQIIPGSSKWEVQSKANHLINTFGMYRCTIQLQSYRQEVDR 420

Qy 421 CANCOSSSP 429

Db 421 CANCOSSSP 429

```

RESULT 12
US-10-024-652-2580
; Sequence 2580, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Eiana
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; TITLE OF INVENTION: Detection of Cancer
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024,652
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/2556,210
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2580
; LENGTH: 428
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-2580

```

Query Match	99.7%	Score 2176;	DB 15;	Length 428;
Best Local Similarity	100.0%;	Prod. No. 1.8e-217;		
Matches 428;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAGSGAMKRLKSMRLKDDAPLFLNDTISAFDPSDEAGDEGLSRFNKRLRVVVAADGSEAPER	60	
Db	1	MAGSGAMKRLKSMRLKDDAPLFLNDTISAFDPSDEAGDEGLSRFNKRLRVVVAADGSEAPER	60	
Qy	61	PVNGAHTLQADDSLLDQDLPITNSQLSLKVDSCDNCCKOREILKQKVKARLITIAVL	120	
Db	61	PVNGAHTLQADDSLLDQDLPITNSQLSLKVDSCDNCCKOREILKQKVKARLITIAVL	120	
Qy	121	YLLEWIGELVGGYIANSIAIMTDALHMLTDLISAILLTLLALWLSKSPKFTFGFHRLE	180	
Db	121	YLLEWIGELVGGYIANSIAIMTDALHMLTDLISAILLTLLALWLSKSPKFTFGFHRLE	180	
Qy	181	VLSAMISVLLVYILMGFLLYEAIVORTIHMYEINGDIMLITAAVGVAVNVIMGFLLNQSG	240	
Db	181	VLSAMISVLLVYILMGFLLYEAIVORTIHMYEINGDIMLITAAVGVAVNVIMGFLLNQSG	240	
Qy	241	HRHSHSLPNSPTRSGCCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAYIIRFKPE	300	
Db	241	HRHSHSLPNSPTRSGCCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAYIIRFKPE	300	
Qy	301	YKIADPICTYVFSLLVATFTFRIIWDVTVIILEGVPSHLVNDYIKEALMKIEDVYSVDL	360	
Db	301	YKIADPICTYVFSLLVATFTFRIIWDVTVIILEGVPSHLVNDYIKEALMKIEDVYSVDL	360	
Qy	361	NIWSLTGSKSTAIWHIQLIPGSSSKWEVQSKANHELLINTFGMYRCTLQLOSRYQEVDR	420	
Db	361	NIWSLTGSKSTAIWHIQLIPGSSSKWEVQSKANHELLINTFGMYRCTLQLOSRYQEVDR	420	
Qy	421	CANCOSSS 428		
Db	421	CANCOSSS 428		

RESULT 13
US-10-012-697-1545
; Sequence 1545, Application US/10012697
; Publication No. US20030215803A1

[illegible]

Query Match	99.2%;	Score 2166.5;	DB 15;	Length 430;
Best Local Similarity	99.5%;	Pred. No. 1.8e-216;		
Matches 428; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1;
Qy	1	MAGSGAWKRLKMLRXDDAPLFNDTSAPDFSDEAGDEGLSRNKLRVVVVADDSSEAPER	60	
Db	1	MAGSGAWKRLKMLRXDDAPLFNDTSAPDFSDEAGDEGLSRNKLRVVVVADDSSEAPER	60	
Qy	61	PVNGAHTPTLQADDSDLLDODPLPTNSQLSLKVDSCNCSKQREILKORKVKARLTIAA	120	
Db	61	PVNGAHTPTLQADDSDLLDODPLPTNSQLSLKVDSCNCSKQREILKORKVKARLTIAA	120	
Qy	121	YLFPMTGELGVGGYIANSIAIMTDALHMLTDLSAIITLLALWLSSSKSPTKRFFGPHRL	- 179	
Db	121	YLFPMTGELGVGGYIANSIAIMTDALHMLTDLSAIITLLALWLSSSKSPTKRFFGPHRL	180	
Qy	180	EVLISAMISVLLVYILMGFLLYEAVQRTIHNNYFINGDIMLITAAVGAVNVVINGFILLNQS	239	
Db	181	XVLISAMISVLLVYILMGFLLYEAVQRTIHNNYFINGDIMLITAAVGAVNVVINGFILLNQS	240	

QY 240 GHRHSHSLPSNPTGSGCERHGHQDSLAVERAAAFVHALGDLVQSVGVLIAYIIRFKP 299
DB 241 GHRHSHSLPSNPTGSGCERHGHQDSLAVERAAAFVHALGDLVQSVGVLIAYIIRFKP 300
QY 300 EYKADPCTVVFSLVAFVTFRIIWDVTVIIIEGVPSHLNVDYIKEALMKIEDVYSVED 359
DB 301 EYKADPCTVVFSLVAFVTFRIIWDVTVIIIEGVPSHLNVDYIKEALMKIEDVYSVED 360
QY 360 LNIWLSLTKGKTAIVHQLIPGSSKWEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 419
DB 361 LNIWLSLTKGKTAIVHQLIPGSSKWEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
QY 420 TCANCQSSP 429
DB 421 TCANCQSSP 430
RESULT 14
US-10-024-652-2581
; Sequence 2581, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Eliana
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; TITLE OF INVENTION: Detection of Cancer
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024,652
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,210
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2581
; LENGTH: 429
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-2581
Query Match 91.2%; Score 1990.5; DB 15; Length 429;
Best Local Similarity 90.7%; Pred. No. 3.8e-198;
Matches 390; Conservative 19; Mismatches 18; Indels 3; Gaps 2;
QY 1 MAGSGANKRLKSLMRKDDAPLNDTSAPDFDEAGDEGLSRFNKLRVVDGSEAPER 60
DB 1 MAGFGANKRLKSLMRKDDAPLNDTSAPDFDEAGDEGLSRFNKLRVVDGSEAPER 60
QY 61 PVNGAHTLQADDLSLDQDLPLTNSQLKVDSCNCSKQRIILKQKVKARLTAAVL 120
DB 61 PVNGAHPALQADDLSLDQDLPLTNSQLKVDSCNCSKQRIILKQKVKARLTAAVL 120
QY 121 YLLEPMIGELVGGYVANSIAIMTALHMLTDLISAILTLALWLSKSPKTRFTFGFHRLE 180
DB 121 YLLEPMIGELVGGYVANSIAIMTALHMLTDLISAILTLALWLSKSPKTRFTFGFHRLE 180
QY 181 VLSAMISVLLIYVLMGFLLEAVQRTTHMNYEINGDMLTAAVGVAVNVIMGFLNQSG 240
DB 181 VLSAMISVLLIYVLMGFLLEAVQRTTHMNYEINGDMLTAAVGVAVNVIMGFLNQSG 240
QY 241 HRHS--HSHSLPSNPTGSGCERHGHQDSLAVERAAAFVHALGDLVQSVGVLIAYIIRFK 298
DB 241 HRHSHSLPSNPTGSGCERHGHQDSLAVERAAAFVHALGDLVQSVGVLIAYIIRFK 299
QY 299 PEYKIADPCTVVFSLVAFVTFRIIWDVTVIIIEGVPSHLNVDYIKEALMKIEDVYSVE 358

DB 300 PEYKIADPCTVVFSLVAFVTFRIIWDVTVIIIEGVPSHLNVDYIKEALMKIEDVYSVE 359
QY 359 DNIWLSLTKGKTAIVHQLIPGSSKWEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 418
DB 360 DNIWLSLTKGKTAIVHQLIPGSSKWEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 419
QY 419 RTCANCQSSS 428
DB 420 RTCANCQSSS 429
RESULT 15
US-09-954-342-37
; Sequence 37, Application US/09954342
; Publication No. US20030170838A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, VISHNU S.
; APPLICANT: SPYTEK, KIMBERLY ANN
; APPLICANT: TAUPIER, RAYMOND J.
; APPLICANT: VERNET, CORINE A.
; APPLICANT: COLMAN, STEVEN D.
; APPLICANT: GORMAN, LINDA
; APPLICANT: TCHERNEV, VELIZAR T.
; APPLICANT: MALYANKAR, URIEL M.
; APPLICANT: SHENOY, SURESH
; APPLICANT: PADIGARU, MURALIDHARA
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENNDA
; APPLICANT: MILLET, ISABELLE
; APPLICANT: PEYMAN, JOHN
; APPLICANT: STONE, DAVID
; APPLICANT: GUNTHER, ERIK
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: LI, LI
; APPLICANT: RASTELLI, LUCA
; APPLICANT: ZERHUSEN, BRYAN
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 21402-114
; CURRENT APPLICATION NUMBER: US/09/954,342
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,382
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/240,498
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/260,284
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/260,973
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/264,794
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/238,398
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/232,675
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/274,862
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/233,801
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,676
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/233,960
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,402
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/233,521
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/233,522
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,679
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 104

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-354-342-37

Query Match          34.2%; Score 747; DB 10; Length 359;
Best Local Similarity 42.0%; Pred. No. 1.1e-68;
Matches 148; Conservative 78; Mismatches 108; Indels 18; Gaps 4;

Qy 82 PLTNSQLSKVDSCDNCSCOREI-----LKQKVKARLTIAAVLYLLFMIGELVGGYIAN 136
Db 20 PVNLPSVELAVQSNHYCHACKDSGSHPNSEKQARRKLYVASAICLVFMIGELVGGYLAQ 79
Qy 137 SLAIMTDALHMLTDLGAILLTLLALWLSKSPKRFPTFGFHRLEVLVSAMISVLLVYILMG 196
Db 80 SLAIMTDAHLLTDFASMLISLSFLWVSRPATKTNFGQRAEILGALLSVLSIWVVTG 139
Qy 197 FLYEAVQRTIHMNYEINGDIMLITAAVGAVNVNMGFLNQSGHRHSHSLPNSPTR 256
Db 140 VLVYLAQRLISGDEYIKGDTMLITSGCAVANIIIMGLALHQSGHGHSHGHSHEDSS--- 196
Qy 257 GSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAVITRFKPEYKIADPICIYVFSLAV 316
Db 197 -----QQQONPSVRAAFIHVVGDLLQSVGVLVAAVYIFKPEYKYVDPICYLFSLIV 249
Qy 317 AFTTFRIIMDVIIIEGVPSHLNVDYIKELMKIEDVYSVEDLNISLTSKGKSTAIVHI 376
Db 250 LGTTLTILRDVILVLMBSGTPKGVDFTTVKNLLSVDGVEALHSLHIWALTVAQPVLVSHI 309
Qy 377 QLIPGSSSKWEVQSKANHLLNTPFGMYRCTIQLOSYRQEVDRTCANCQSS 428
Db 310 AIAQNDA--QAVLKVARDELQGFNFHTMTIQIESYSDM-KSCQECQGPS 358
```

Search completed: July 29, 2004, 17:46:17
Job time : 48 secs

Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 17:40:40 ; Search time 39 Seconds
(without alignments)
3470.700 Million cell updates/sec

Title: US-10-024-652-2570

Perfect score: 2183

Sequence: 1 MAGSGAWRLKSLMRKDDAP.....LQSYROEVDRTCANCOSSSP 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2183	100.0	429	4	Q8TC39
2	742	34.0	146	4	Q96J77
3	652.5	29.9	472	5	Q9V471
4	648.5	29.7	369	4	Q8IWA4
5	643.5	29.5	367	11	Q8BGG0
6	638.5	29.2	382	5	Q22541
7	638	29.2	320	4	Q8TCL3
8	627	28.7	440	5	Q8IP48
9	615	28.2	388	4	Q8TC03
10	607.5	27.8	410	5	Q45923
11	603.5	27.6	391	5	Q45922
12	599.5	27.5	669	5	Q9VKA3
13	565.5	25.9	498	5	Q8T0G1
14	555	25.4	398	10	Q81036
15	547	25.1	398	10	Q9ZT63
16	546	25.0	392	10	Q94B00

17	543.5	24.9	396	10	Q93XE9
18	539	24.7	323	4	Q9BRI3
19	537.5	24.6	418	10	Q84NH0
20	536.5	24.6	421	10	Q947R8
21	534	24.5	385	10	Q9ZWC3
22	532	24.4	378	10	Q9LXS1
23	530	24.3	360	10	Q94A29
24	526.5	24.1	334	10	Q9M271
25	469.5	21.5	334	5	Q8SQT3
26	453	20.8	299	16	Q81F93
27	446	20.4	299	16	Q81SA9
28	444.5	20.4	300	16	Q8ERA7
29	440.5	20.2	319	16	Q8NVN6
30	437.5	20.0	319	16	Q99X53
31	429	19.7	556	5	Q8IBU1
32	418.5	19.2	313	16	Q8CPX7
33	407	18.6	308	16	Q67168
34	399.5	18.3	317	2	Q05214
35	396.5	18.2	316	2	Q9R494
36	391	17.9	303	16	Q8Y480
37	387	17.7	303	16	Q927R8
38	385	17.6	313	16	Q83SA2
39	384.5	17.6	371	16	Q826X7
40	383.5	17.6	317	16	Q8F433
41	380.5	17.4	301	16	Q88RV3
42	377	17.3	297	16	Q83EH0
43	376.5	17.2	449	5	Q9VZR4
44	372.5	17.1	323	16	Q8CNH2
45	370	16.9	311	16	Q07084

ALIGNMENTS

RESULT 1

ID	Q8TC39	PRELIMINARY;	PRT;	429 AA.
AC	Q8TC39;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)			
DE	Solute carrier family 30 (Zinc transporter), member 4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RA	Strausberg R.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC026089; AAH26089.1; -			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0008324; F:cation transporter activity; IEA.			
DR	GO; GO:0008612; P:cation transporter; IEA.			
DR	InterPro; IPR002524; Cation efflux.			
DR	Pfam; PF01545; Cation efflux; 1.			
DR	TIGRFAMs; TIGR01297; CDF; 1.			
SQ	SEQUENCE 429 AA; 47482 MW; 9737FCBE881C8C32 CRC64;			

Query Match	100.0%;	Score 2183;	DB 4;	Length 429;
Best Local Similarity	100.0%;	Pred. No. 5.6e-183;	Mismatches 0;	Gaps 0;
Matches 429;	Conservative 0;			
QY	1	MAGSGAWRLKSLMRKDDAPFLNDTSAPDFSDAGDEGLSRFNKLVRVVVADGSEAPER	60	
Db	1	MAGSGAWRLKSLMRKDDAPFLNDTSAPDFSDAGDEGLSRFNKLVRVVVADGSEAPER	60	
QY	61	PVNGAHTPTQADDDSLLDQDLPTNSQLKVDSCDNCQKREILKQKVKARLTAAYL	120	
Db	61	PVNGAHTPTQADDDSLLDQDLPTNSQLKVDSCDNCQKREILKQKVKARLTAAYL	120	
QY	121	YLLFMIGELVGGVIANSLAINTMDALHMLTDLISAILLTLLWLSSKSPTKRFTFGFGRLE	180	


```
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.I., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreshek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003646; AAF53443.1; -
DR EMBL; AE003412; AAF4926.1; -
DR EMBL; AY071460; AAL49082.1; -
DR Flybase; FBgn028516; BG:DS07295.1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002524; Cation_efflux.
DR Pfam; PF01545; Cation_efflux; 1.
DR TIGRFAMs; TIGR01297; CDF; 1.
SQ SEQUENCE 472 AA; 51036 MW; 077037ACFAAE3BF5 CRC64;

Query Match 29.9%; Score 652.5; DB 5; Length 472;
Best Local Similarity 31.1%; Pred. No. 1.4e-48;
Matches 155; Conservative 91; Mismatches 135; Indels 117; Gaps 12;

QY 13 MLRKDDAPLFNDTSAPDFSD-----EAGDEGLSRFNKLRVVVADGSEAPERPV 62
DB 1 MSRNEDTPIAKDSGRTRRSNYGTAPSFHLMQOQGVN-----VVAGNG----- 45

QY 63 NGAHPTQADDSDLLDQDLPLTNSQL-----SLKVDSCNCKSKORILKQKVKARLTI 116
DB 46 NNHHPA-----TPATPAQIFCLHGRSNNEVRDCHHRSSEGVNDVXARRKLLI 93

QY 117 AAVLYLFLMIGELVGGYIANSIAIMTDALHMLTDLSAIITLLALMLSSKSPTRKFTFFG 176
DB 94 ASILCLAVFMIAEIVGGVLSLSLATDAHLLTDFASFMSLSLFAIWIAGRPSTQMSFGW 153

QY 177 HRLVLSAMSVLLVYILMGFLLYEAVQRTIHNNYINGDIIMLITAAVGVANVINGFLL 236
DB 154 YRAEIVGAMASVFMIVITGLVLAIGRLISGDEYVNAKIMLTISGLAILVNVINGVOL 213

QY 237 NQ-----SCHRHSH-----SHSLPSNSPTRSGGCR----- 262
DB 214 QGHSHGLGGHSHGSKGNASVQVATSPCSQSPQRLEGVAVAPDAELPGGLPT 273

QY 263 -----NHGQD-----SLAVRAAFVHALGDLVQSVG 287
DB 274 PSYQNTKLVDPTDLEIAAVLAETAAPGSHRHGPGVGREAVNMNVRAALIHVIGDVQSVG 333

QY 288 VLIIRKPEKPIKADICTYVFSLLVAPTFRITWDVTVILLEGVPSHLAVNDYIKEA 347
DB 334 VFVAGVYFVPEYSVDICTYVFSLLVAPTFRITWDVTVILLEGVPSHLAVNDYIKEA 393

QY 348 LMKIEDVYVSDNLNWSITSGKSTAIVHIQILPGSSSK-WEVQSKANHLILNTFGMYRC 406
DB 394 FQIEGVERVENLRIWALSINKVALSAHLAENANPKRILDAATSAVHLRYNFF--ET 450

QY 407 TIQLOSRQEVDRTCANC 424
DB 451 TIQIEDYTAQME-SCLOC 467

RESULT 4
Q81WU4 PRELIMINARY; PRT; 369 AA.
AC Q81WU4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
RX MEDLINE=22354683; PubMed=12466851;
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
```

```
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Zinc transporter Znt-8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Seve M., Davenegnas S., Chiment F., Chantegrel J., Favier A.;
RT "Znt-8, a pancreatic specific zinc transporter.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV117411; AAM80562.1; -
DR Genew; HGNC:20303; SLC30A8.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002524; Cation_efflux.
DR Pfam; PF01545; Cation_efflux; 1.
DR TIGRFAMs; TIGR01297; CDF; 1.
SQ SEQUENCE 369 AA; 40728 MW; A568300E83DCBB22 CRC64;

Query Match 29.7%; Score 648.5; DB 4; Length 369;
Best Local Similarity 38.0%; Pred. No. 2.3e-48;
Matches 139; Conservative 75; Mismatches 107; Indels 45; Gaps 6;

QY 83 LTNSQLSLKVDSCNCKSKOR-EILKQ-----RKVKARLTIAAVLY 121
DB 22 LSEVLEQQPVNKDQCPREPELESQGMHCHSGKTEKGANAYAKWKLCSASAIC 81

QY 122 LFMIGELVGGYIANSIAIMTDALHMLTDLSAIITLLALMLSSKSPTRKFTFFGHRLEV 181
DB 82 FIFMIAEVVGGIAGSLAVVTDAAHLITDLTSLFLSLWLSKPPSKRLTFGWHRAEI 141

QY 182 LSAMISVLLVYILMGFLLYEAVQRTIHNNYINGDIIMLITAAVGVANVINGFLLNQS-- 239
DB 142 LGLALSLICIVVTVGLVYLACERLLYDYQIQATVMIIVSSCAVAAIVLTVLHQRL 201

QY 240 GHRHSHSLPSNSPTRSGGCRNHGQDSLAVRAAFVHALGDLVQSVGLIAAYIIRFKP 299
DB 202 GHNHKEV-----QANASVRAAFVHALGDLFQSLVLSALIIYFKP 242

QY 300 EYKIADPCTYVFSLLVAPTFRITWDVTVILLEGVPSHLNVDYIKEALMKIEDVYVSD 359
DB 243 EYKIADPCTYVFSLLVAPTFRITWDVTVILLEGVPSHLNVDYIKEALMKIEDVYVSD 302

QY 360 LNIWSITSGKSTAIVHIQILPGSSSKWEVQSKANHLILNTFGMYRCITQLOSRQEVDR 419
DB 303 LHWLSLTMQVLSAHVATAASRDS--QVRRRIAKALSKSFTMSLTIQMES-PVDQDP 359

QY 420 TCANCO 425
DB 360 DCLFCE 365

RESULT 5
Q8BGG0 PRELIMINARY; PRT; 367 AA.
ID Q8BGG0;
AC Q8BGG0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Weakly similar to zinc transporter 2.
GN C820002P14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=22354683; PubMed=12466851;
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
RA The FANTOM Consortium,
```

RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK050482; BAC34281.1; -.
 DR EMBL; AK050494; BAC34289.1; -.
 DR MGD; MGI:2442682; C820002P14Rik.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002524; Cation efflux.
 DR Pfam; PF01545; Cation_efflux; 1.
 DR TIGRFAMs; TIGR01297; CDF; 1.
 SQ SEQUENCE 367 AA; 40222 MW; 9C9484A561DB58E4 CRC64;
 Query Match 29.5%; Score 643.5; DB 11; Length 367;
 Best Local Similarity 38.8%; Pred. No. 6.2e-48;
 Matches 130; Conservative 81; Mismatches 97; Indels 27; Gaps 5;
 QY 95 CDNCSKQ--REILKQKVKARLTIAAVLYLLFMIGELVGGYIANSIAIMTDALHMLTDL 152
 Db 52 CHNSAKATGNRSSKQAHAKWRLCAASAICTIFWVAEVVGGHVAGSLAILTDAAHLLIDL 111
 QY 153 AIITLALWSSKSPKRTFGFHRLEVLAMISVLLVILMGFLLYEAVQRTIHWYE 212
 Db 112 SFLLSLFSLWSSRPPSKRLTFGWYRAAILGALLSVLCIWWTVGLLYLACERLLYPDQ 171
 QY 213 INGDMILITAAVGVANVIMGFLNQSHRSHSLPNSPTRSGCERNHQDQLAVR 272
 Db 172 IQAGIMTVSCAAVAILVTMLHQRNFYGNHCV-----QANASVR 214
 QY 273 AAFVHALGDLVQSVGVLIAAVITRKPEYKIADICTYVFSLLVAFTHRIIWDTVIIL 332
 Db 215 AAFVHALGDLVQSVGVLIAAVITRKPEYKIADICTYVFSLLVAFTHRIIWDTVIIL 274
 QY 333 EGVPSHNLNDYIKALMKIEDVSVEDLNWLSLTSGKSTAIHQLIPGSSKWEVSQSK 392
 Db 275 EGVPSGLSYNSVKELIIVADGVISVHSLHLSLTVQVLSVHV-----ATAASQDSQSV 329
 QY 393 ANHL--LNTFGMYRCTIQSVRQEVDRTCANQ 425
 Db 330 RTGIAQALSSPDLHSLTIQIESAADQ-DPSCLICE 363
 RESULT 6
 Q22541 ID Q22541 PRELIMINARY; PRT; 382 AA.
 AC Q22541;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE T18D3.3 protein.
 GN T18D3.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA note;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z68119; CAA92193.1; -.
 DR PIR; T24963; T24963.
 DR WormPep; T18D3.3; CE03664.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002524; Cation efflux.
 DR Pfam; PF01545; Cation_efflux; 1.
 DR TIGRFAMs; TIGR01297; CDF; 1.
 SQ SEQUENCE 382 AA; 42237 MW; 44A02AEF60B89484 CRC64;
 Query Match 29.2%; Score 638.5; DB 5; Length 382;
 Best Local Similarity 39.8%; Pred. No. 1.8e-47;
 Matches 136; Conservative 70; Mismatches 105; Indels 31; Gaps 8;
 QY 91 KVDSCNCSKOREILKQKVKARLTIAAVLYLLFMIGELVGGYIANSIAIMTDALHMLTD 150
 Db 59 EADSTDSDH-----SNRRATRIILWLVLCFFWVCEVIGVLAGSLAIVTDAHLTD 112
 QY 151 LSAIILTLALWSSKSPKRTFGFHRLEVLAMISVLLVILMGFLLYEAVQRTIHMN 210
 Db 113 FASVLISLFSLYIARRPPSQKMSFGFHEAVLGAFFSVFLIWIIVTVGLVLAIMRIYSGD 172
 QY 211 YEINGDIMLITAAVGVANVIMGFLNQSHRSHSLPNSPTRSGCERNHQ----- 266
 Db 173 YEVEGGIMALTAAALGVVNVLMALLYFGHSHSH-----GGGSHSHSHGCGN 221
 QY 267 -DSLAVRAAFHALGDLVQSVGVLIAAVITRKPEYKIADICTYVFSLLVAFTHRII 325
 Db 222 GDNINVRAAFHVGLDLSGLVLAALFIYFQSWIIDPCTLVFSVIVLCTIILR 281
 QY 326 DTWIIILGVPSHNLNDYIK--EALMKIEDVSVEDLNWLSLTSGKSTAIHQLIPGSS 383
 Db 282 DAMIVLLEGSP--NIDFAKVFSSLEDIEGVKVKHDLRIWLSLTKIALSVHLEIDANSQ 339
 QY 384 SKWEVQSKANHLILNTFGMYRCTIQSVRQEVDRTCANQ 424
 Db 340 S--QSILRETRKMLKQTVNVEHTIQIEEF--GANRSDCGKC 377
 RESULT 7
 Q8TCL3 ID Q8TCL3 PRELIMINARY; PRT; 320 AA.
 AC Q8TCL3;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN DKFZP564F1062
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL713790; CAD28545.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002524; Cation efflux.
 DR Pfam; PF01545; Cation_efflux; 1.
 DR TIGRFAMs; TIGR01297; CDF; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 320 AA; 35053 MW; 5D7325EBD1758EC9 CRC64;
 Query Match 29.2%; Score 638; DB 4; Length 320;
 Best Local Similarity 41.0%; Pred. No. 1.6e-47;
 Matches 130; Conservative 69; Mismatches 94; Indels 24; Gaps 4;
 QY 111 KARLTIAAVLYLLFMIGELVGGYIANSIAIMTDALHMLTDL 170
 Db 22 KWKLSASAICFIFMIAEVGGHAGSLAVVYDAHLLIDLTSLFLLSFLSLSKPPSK 81
 QY 171 RFTFGFHEVLAMISVLLVILMGFLLYEAVQRTIHMNVEINGDMILITAAVGVANV 230

```

Db 82 RLTFGWHRABEILGALLSILCIWVTVGVLYVYLACERLLYPDYQIQATVMIIVSSCAVAANI 141
Qy 231 IMGELLNQS--CHRHSHSLPSNSPTRGSCERNHGQDSLAVRAAFVHALGDLVQSGV 288
Db 142 VLTVLVLRQRCUHNHEV-----QANASRAAFVHAPGLFOSISV 182
Qy 289 LIAAYIRFKEPKYIADPICTYVFSLLVAFVTFRIIWDTVVILEGVPSHLVNDYIKEAL 348
Db 183 LISALIYFKEPKYIADPICTFISILVASTITILADFSILLMEGVPKSLNYSVGKELI 242
Qy 349 MKIEDVSVDELNWSITSGKSTAIHVLIQIPGSSKWEVQSKANHLINTTGMVACTI 408
Db 243 LAVDGVLSVHCLHWSITMNVQVILSAHVATAASRDS--QVRRRIAXAKSKSTWRSITI 300
Qy 409 QLOQSVROEVDRTCANCO 425
Db 301 QMES-PVQDDPDLFCF 316

RESULT 8
C8IP48
ID Q8IP48 PRELIMINARY; PRT; 440 AA.
AC Q8IP48;
DT 01-MAR-2003 (TRENBLREL 23, Created)
DT 01-JUN-2003 (TRENBLREL 23, Last sequence update)
DT 01-JUN-2003 (TRENBLREL 23, Last annotation update)
DE CG3994-PB.
GN BG:DS07295.1 OR CG3994.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.J., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abiril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foltier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."

```

```

RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA Pacieb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003646; AA010893.1; -; Length 440;
DR Flybase; FBgn0028516; BG:DS07295.1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002524; C:cation efflux.
DR Pfam; PF01545; C:cation efflux; 1.
DR TIGRPFAM; TIGR01297; CDF; 1.
SQ SEQUENCE 440 AA; 47993 MW; 82E291198572C76C CRC64;
Query Match 28.7%; Score 627; DB 5; Length 440;
Best Local Similarity 33.6%; Pred. No. 2.2e-46;
Matches 134; Conservative 81; Mismatches 110; Indels 74; Gaps 7;
Qy 96 DMSKQREILKORKVKARITIAAVLYLLFMIGELVGGVIANSLAINTALHMLTDLIAII 155
Db 41 DCHRRARSEGVDVKARRKLIITIASILCLVFMIAEIVGGVLSLAITADAAHLITDFA 100
Qy 156 LTLTALWSSKSPTRFTFGFHLRLVLSAMISLVLLVYLMGLFLYEAQVORTHMYNEING 215
Db 101 ISLFAIWIAGRSTORMSGFVRAEIVGAMASVFMIVITGLIWLALCRLLSGDYEVNA 160
Qy 216 DIMLITAAVGVAVNVINGFLNQ-----SCHRHSH-----SHSLPSNSPTRSGGCR 262
Db 161 KIMLITGLAILVNVIMGVQLQHGHSHGLGGHSHGSGKNASHVQATSTPCSDSPSQR 220
Qy 263 -----NHGQD----- 267
Db 221 IEGGVAYAPEDAELPGGLPTFSYQNTKLVPTLDEIAAVLAETAPGSHHGGVGRE 280
Qy 268 -SLAVRAAFVHALGDLVQSGVLIYAAYIRFKPEYKIADPICTYVFSLLVAFVTFRIIWD 326
Db 281 VNMVRAALIHVIGDVGISGVGFVAAGVYEFWPEYSIVDPICTFVFSIIVLFTFTIMKD 340
Qy 327 TVVILEGVPSHLVNDYIKBALMKITDYVSVEDLNINSLTSGKSTAIHVLIQIPGSSSK- 385

```

```
Db 341 ALLVMEGTPTNMYAEVQLFQIEGVERVHNRIRIWAISINKVALSAHLAIAENANPKR 400
QY 386 WEEVQSKANHLNLTFGMYRCTIQLQSYRQEVDRTCANQ 424
Db 401 ILDAATSAVHLRYNFF---ETTIQIEDYTAQME-SCLQC 435

RESULT 9
Q8TC03 ID Q8TC03 PRELIMINARY; PRT; 388 AA.
AC Q8TC03
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Solute carrier family 30 (zinc transporter), member 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028358; AAR28358.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002524; F:cation transport; IEA.
DR Pfam; PF01545; Cation_efflux; 1.
DR TIGRFAMs; TIGR01297; CDF; 1.
SQ SEQUENCE 388 AA; 41945 MW; D73DE56P46860FD8 CRC64;

Query Match 28.2%; Score 615; DB 4; Length 388;
Best Local Similarity 37.2%; Pred. No. 2.1e-45;
Matches 130; Conservative 80; Mismatches 133; Indels 6; Gaps 4;

QY 79 QDLPLTNSQLSKVDSKQREILKQKVKAR--LTIAAVLYLLFMIGELVGGYIAN 136
Db 39 EPLPEESKPVEMPHHCHDPLPPGLTPERLHARRQLYAAACAVCFVFMAGEVGGYLAH 98
QY 137 SLATMTDALMLTDLIAIITLLALWLSKSPKPTFGFHRLEVLISAMISLVLLVILMG 196
Db 99 SLAINTDAHLADVGMSGSLFSLMLSTRPATRTMTFGWHRSETGALASVVSLLMWVTG 158
QY 197 FLLYEAVQRTIHMNYEINGDIMITAAAGVANVINGFLNQSGHRSHSHSLFNSPTR 256
Db 159 ILLYLAFLRLHSDYHIEGGMLLTASIVCANLLMAFVLHQAGPPHSHGSRGAEPAPLE 218
QY 257 GSGCERNHGQDSLAFAAFVHALGDLVQSGVGLIAAVIIRFPEYKIADPCTYVFSLLV 316
Db 219 -EGPEEPLPLGNTSVRAAFVHLGDLQSGFGLAASILIYFKPKQYKAADPISTFLPSICA 277
QY 317 AFTTFRIIWDVTWIILEGVPSHLNVDYIKALKMKIEDVYSVEDLNINWLSLTSKSTAIVHI 376
Db 278 LGSTAPILRDVIRILMGTPRNVGPEPVDTLLSVPGVRATHLHLWALTITVHVASAHL 337
QY 377 QLIPGSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDRTCANQ 425
Db 338 AI--DSTADPAVLAESAASSRLSYRFGFSCTQLQVEQYQPEMAQ-CLRCQ 383

RESULT 10
ID O45923 PRELIMINARY; PRT; 410 AA.
AC O45923;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Y39E4A.2b protein.
GN Y39E4A.2 OR Y39E4A.2B.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
```

```
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL021480; CAA16328.1; -.
DR PIR; T26757; T26757.
DR WormPep; Y39E4A.2b; CE16617.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002524; Cation_efflux.
DR Pfam; PF01545; Cation_efflux; 1.
DR TIGRFAMs; TIGR01297; CDF; 1.
SQ SEQUENCE 410 AA; 44082 MW; 8379EA941809270C CRC64;

Query Match 27.8%; Score 607.5; DB 5; Length 410;
Best Local Similarity 37.7%; Pred. No. 1e-44;
Matches 130; Conservative 76; Mismatches 114; Indels 25; Gaps 6;

QY 93 DSCDNC-----SKQREILKQKVKARLTIAAVLYLLFMIGELVGGYIANSLAINT 142
Db 74 DSSDCSGAGGGAHKHSHDEYKQKRAEKVLAVALSAVFAAEFVGGFWAQSLAINT 133
QY 143 DALHMLTDLIAIITLLALWLSKSPKPTFGFHRLEVLISAMISLVLLVILMGFLLYEA 202
Db 134 DAGHMLDLSLFIISIFAIRCARLPASKRLSGYERAEVLGALTSVILWLTTLVWVA 193
QY 203 VORTIHMNYEINGDIMITAAAGVANVINGFLNQSGHRSHSHSLFNSPTRGSCER 262
Db 194 IQRIVNNHEDVADVMLITAGVGLFVNLVGLFVGTGGHGHTH-----GGHSH 244
QY 263 NHGQD--SLAVRAAFVHALGDLVQSGVGLIAAVIIRFPEYKIADPCTYVFSLLVAFTT 320
Db 245 GHADGKNVNVRAALHIVIGLVQSGVGLIAALIRF-TGWTLADPCTFLFSIIVLFTT 303
QY 321 FRIIWDVTWIILEGVPSHLNVDYIKALKMKIEDVYSVEDLNINWLSLTSKSTAIHQIIP 380
Db 304 VTWRDIEFVLMEATPSSHVDLSVKKALSALLEGYKGVHDLHLSIGMDKTAFSVHLAL-- 361
QY 381 GSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDRTCANQ 425
Db 362 ESPNRMENVAEASRLIRRGVAVATVQVEPFDEKID-SCDTQC 405

RESULT 11
ID O45922 PRELIMINARY; PRT; 391 AA.
AC O45922;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Y39E4A.2a protein.
GN Y39E4A.2 OR Y39E4A.2A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
```



```
[6]
RN  SEQUENCE FROM N.A.
RP  FlyBase;
RA  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY069340; AAL39485.1; -
DR  EMBL; AY003785; AAM68358.1; -
DR  FlyBase; FBgn025693; BESI:CK02137.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0008324; F:cation transporter activity; IEA.
DR  GO; GO:0006812; P:cation transport; IEA.
DR  InterPro; IPR002524; Cation efflux.
DR  Pfam; PF01545; Cation efflux; 1.
DR  TIGRFAMs; TIGR01297; CDF; 1.
SQ  SEQUENCE 498 AA; 55014 MW; AE0161C0DC3654E8 CRC64;

Query Match      25.9%; Score 565.5; DB 5; Length 498;
Best Local Similarity 29.3%; Pred. No. 6.6e-41;
Matches 134; Conservative 91; Mismatches 155; Indels 77; Gaps 8;

QY  25  DTSAFDSDEAGDEGLFRKLRVAVVADGSEAPERFVNGAHPTIQADDSDLLDQLPLT 84
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  85  NSQLSKVDSDCNCSKOREILKOR---KVAKRLTIAAVLYLLEFMIGELVGGYIANSIAIM 141
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  101  ETEFDMQRECNHOPGFRANSKSKSAOEAQYKIMLAVALCCVFMIEFLGGYVAGSLAIM 160
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  142  TDALHMTDLSAILTLTLLALWLSKSPKPTFGFHRLEVLVSAMISVLLVYILMGFLIVE 201
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  161  TDAHLASDCISFVIGVAVTWIGRPDPDRMSFGYKRFVIGALASILGFTVFTLLVVV 220
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  202  AVORTIHMYEINGDIMLIITAAVGVAVNVIMGFL-----NOSGRHSHSHSLPNSPT 255
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  221  AIERIFQDFELNADMMMLISGIGIVINVMFVLHGSWFVNGHGHSHSHS-HSHSHS 279
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  256  RGSCERN----- 263
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  280  HNGHEPNDSLSQTRSNSEFLTITIGSQSASTADEDSIRKEINSNEKIVITNGKKPTLT 339
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  264  -----HGQDSLAVRAAFVHALGDLVQSVGLIAAVIIRFKPEYKIADPTICTYVFSLL 315
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  340  GTSNNELAHEDKNLNRAMHIVGDLVQSIGVFLAAVLIKVCPGAKYADPLCTLIFSII 399
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  316  VAFPTFRRIIWDTVIILEGVPSHLNVDIKEALMKIEDVYSVEDLNWISLTSKSTAIYH 375
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  400  VIMTTLRFRESGLIIVNAVQNLMNMTLHLELGSIEGVSRLHNLNVWQTSQORVLMVH 459
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  376  IQLIPGSSSKWEVQSKANHLIN-TFGMVRCITQLQ 411
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  460  --LVTDGRADGNEVLQAATALVSSPRYNKIHSTIQLE 494
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 14
ID  O81036  PRELIMINARY; PRT; 398 AA.
AC  O81036;
DT  01-NOV-1998 (TrEMBLrel. 08, Created)
DR  01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Putative zinc transporter (ZAT).
GN  AT2G4800.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC  eurosids II; Brassicales; Brassicaceae; Arabidopsids.
CX  NCBI_TaxID=3702;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=cv. Columbia;
RX  MEDLINE=20083487; PubMed=10617197;
RA  Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA  Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA  Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
```

```
RA  Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA  Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA  Copenhagen G.P., Preuss D., Nierman W.C., White O., Bisen J.A.,
RA  Salzberg S.L., Fraser C.M., Venter J.C.;
RT  "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT  thaliana.";
RT  Nature 402:761-768(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=cv. Columbia;
RA  Lin X.;
RL  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RA  Haas B.J., Volfovsky N., Town C.D., Troughan M., Alexandrov N.,
RA  Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT  "Full-length messenger RNA sequences greatly improve genome
RT  annotation.";
RT  Genome Biol. 0:0-0(2002).
RN  [4]
RP  SEQUENCE FROM N.A.
RA  Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA  Feldmann K.;
RT  "Full-length cDNA from Arabidopsis thaliana.";
RL  Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AC005310; AAC33498.1; -
DR  EMBL; AY085033; AAM63243.1; -
DR  FIR; T02681; T02681.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0008324; F:cation transporter activity; IEA.
DR  GO; GO:0006812; P:cation transport; IEA.
DR  InterPro; IPR002524; Cation efflux.
DR  Pfam; PF01545; Cation efflux; 1.
DR  TIGRFAMs; TIGR01297; CDF; 1.
SQ  SEQUENCE 398 AA; 43827 MW; 7E20E0B29237BB23 CRC64;

Query Match      25.4%; Score 555; DB 10; Length 398;
Best Local Similarity 33.8%; Pred. No. 4.1e-40;
Matches 116; Conservative 74; Mismatches 107; Indels 46; Gaps 4;

QY  113  RTIAAVLYLLEFMIGELVGGYIANSIAIMTALHMTDLSAILTLTLLALWLSKSPKRF 172
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  57  KLCIAVAVLCVPMSEVVGKANSALITDAHLSDVAFAISLFSLAGWEATPRQ 116
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  173  TGFHRLEVLVSAMISVLLVYIIMGFLYEAQVORTIHMYEINGDIMLIITAAVGVAVNVIM 232
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  117  TVGFRIELGALVSIQLINLTGLVYEAIRIVTETSEVNGFLMFLVAAFGLVNIIM 176
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  233  GFLLNQS-----CHRHSHSHSLPNSPT-----RSGCERNHGQD----- 267
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  177  AVLLGHGHHGHHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGH 236
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  268  -----SLAVRAAFVHALGDLVQSVGLIAAVIIRFKPEYKIADPTIC 308
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  237  EQLDKSKTQVNAKEKRRKRNINLQAYLHVLGDSIQSVGVWIGGAIWYNPEWKIVDLIC 296
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  309  TVVFSLLVAFPTFRRIIWDTVIILEGVPSHLNVDIKEALMKIEDVYSVEDLNWISLTSG 368
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  297  TLFASVIVLGTITNIRNILEVLMESTPREIDATKLEKGLLEMEERVAWHELHIWATVVG 356
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  369  KSTAIYHQLIPGSSSKWEVQSKANHLINLTTFGMVRCITQLQ 411
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY  357  KVLACHVNIPEADA--DMVLNKVIDYIRREYNISHVTIQIE 397
Db  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 15
ID  Q9ZT63  PRELIMINARY; PRT; 398 AA.
AC  Q9ZT63;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DR  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Zinc transporter ZAT.
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 17:41:15 ; Search time 17 Seconds
(without alignments)
2427.421 Million cell updates/sec

Title: US-10-024-652-2570
Perfect score: 2183
Sequence: 1 MASGAWKLSMLRKDDAP.....LQSYRQEVDRTCANCOSSP 429

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	747	34.2	359	1 S70632	zinc transporter 2
2	638.5	29.2	382	2 T24963	hypothetical prote
3	607.5	27.8	410	2 T26757	hypothetical prote
4	603.5	27.6	391	2 T26756	hypothetical prote
5	555	25.4	398	2 T02681	probable zinc tran
6	534	24.5	385	2 A84696	probable zinc tran
7	532	24.4	378	2 T49164	zinc transporter-1
8	526.5	24.1	334	2 T47986	zinc transporter-1
9	437.5	20.0	319	2 D89778	hypothetical prote
10	407	18.6	308	2 E70392	cation efflux syst
11	391	17.9	303	2 AG1396	cation transport p
12	387	17.7	303	2 AB1772	ybgr protein - Esc
13	386	17.7	313	1 H64810	probable transport
14	385	17.6	311	2 B85577	probable transport
15	385	17.6	313	2 D90726	probable cation tr
16	372	17.0	312	2 A20593	cation-efflux syst
17	370	16.9	311	2 C59612	cation-efflux syst
18	369.5	16.9	325	2 T44365	hypothetical prote
19	369.5	16.9	325	2 G9C008	probable cation ef
20	368	16.9	299	2 C83595	probable efflux pr
21	365.5	16.8	312	2 T35276	cobalt-zinc-cadmium
22	357.5	16.4	301	2 AH3431	probable cation tr
23	355	16.3	312	2 A10138	cadmium, zinc, cob
24	353	16.2	316	1 UC4701	cobalt-zinc-cadmium
25	351.5	16.1	321	2 G82752	probable zinc/cadm
26	343	15.7	387	2 T38252	probable heavy met
27	343	15.7	387	2 T43140	cobalt accumulat
28	343	15.7	439	2 S58327	heavy metal ion re
29	342	15.7	442	2 S56057	

30	341	15.6	303	2 H92122	co/Zn/Cd efflux sy
31	337	15.4	325	2 A75437	cation efflux syst
32	336.5	15.4	300	2 D84459	probable cation tr
33	325.5	14.9	284	2 G72363	cation efflux syst
34	314.5	14.4	304	2 AG2540	probable cation tr
35	306.5	14.0	316	2 E81321	probable cation ef
36	296	13.6	295	2 H71078	zinc transport pro
37	284.5	13.0	507	2 S54303	hypothetical prote
38	282.5	12.9	299	2 F98080	cation efflux syst
39	282.5	12.9	299	2 H95216	zinc transporter 2
40	282.5	12.9	503	2 S54302	cation efflux fami
41	271.5	12.4	361	2 F87286	cation efflux syst
42	264.5	12.1	304	2 G86825	cation efflux syst
43	249	11.4	199	1 D33830	cation-efflux syst
44	248	11.4	281	2 A82161	probable metal tra
45	245.5	11.2	326	2 D83483	

ALIGNMENTS

RESULT 1

S70632
zinc transporter Znt-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: S70632
R:Palmiter, R.D.; Cole, T.B.; Findley, S.D.
EMBO J. 15, 1784-1791, 1996
A:Title: Znt-2, a mammalian protein that confers resistance to zinc by facilitating vesic
A:Reference number: S70632; MUID:96203098; PMID:8617223
A:Accession: S70632
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <PAL>
A:Cross-references: EMBL:U50927; NID:gi256377; PIDN:AAB02775.1; PID:gi256378
C:Genetics:
A:Gene: Znt-2
A:Start codon: CTG
C:Superfamily: zinc transporter Znt-2

Query Match 34.2%; Score 747; DB 1; Length 359;
Best Local Similarity 42.0%; Pred. No. 5.9e-53;
Matches 148; Conservative 78; Mismatches 108; Indels 18; Gaps 4;

QY	82	PLTNSQLSKVDSCNCSKQREI-----LKQKVKARLTIAAVLYLLFMIGELVGGYIAN	136
DB	20	PVNLPSVELAVQSNHYCHQAQKDSGHPNSEKQRRARKLYVSAICLVFMIGIIGYLAQ	79
QY	137	SLAIMTDALHMLTDLISAILLTLALWLSKSPKFTFGFHRLEVLVSAMISVLLVYILMG	196
DB	80	SLAIMTDAHLITDFASMLISLFLWVSSRPATKTNFGWQRAEILGALLSVLSIWWVTG	139
QY	197	FLLYEAVQRTIHMNVEINGDIMLITAAVGVAVNVIMGFLNQSGHRHSHSLSPNSPTR	256
DB	140	VLVYLAVQRLISGDVEIKGDTMLITSGCAVANVIMGLALHQSGHSHSHEDSS---	196
QY	257	SGCERNHQDLSAVRAAFVHALGDLVQSGVGLIAAYIRFPKPKYKADPCTTYVFLSLV	316
DB	197	-----QQQNPSVRAAFIHYVGBLQSGVGLVAAYIYFKPKYKADPCTCTFLSLIV	249
QY	317	ATTFTRIIWDVTVIILEGVPSHLNVDIKEALMKIEDVYVEDLNATWSLTSGKSTAIYHI	376
DB	250	LGTTLTILDLVILVMEGTPKGVDTTVKNLLSLVDGVEALSHLWALTVAQPVLSVHI	309
QY	377	QLIPGSSSSWEVQSKXANHLNTFTGWRCTTQLQSYRQEVDRTCANCOSSS	428
DB	310	ATAQNVA--QAVLKVARDLQCKNFHTMTIIESYSDM-KSQCECGPS	358

RESULT 2

T24963
hypothetical protein T18D3.3 - Caenorhabditis elegans

RESULT 5

T02681
probable zinc transporter At2g46800 [imported] - Arabidopsis thaliana
N/Alternate names: hypothetical protein F19D11.8
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C/Accession: T02681; D84907
R/Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ronsley, S.D.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: T02681

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-398 <ROU>

A/Cross-references: EMBL:AC005310; NID:g3510247; PID:g3510254

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: D84907

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-398 <STO>

A/Cross-references: GB:AB002093; NID:g3510254; PIDN:AAC33498.1; GSPDB:GN00139

C/Genetics:

A/Gene: At2g46800; F19D11.8

A/Map position: 2

Query Match 25.4%; Score 555; DB 2; Length 398;

Best Local Similarity 33.8%; Pred. No. 2.6e-37;

Matches 116; Conservative 74; Mismatches 107; Indels 46; Gaps 4;

Qy 113 RLTAAVLYLLFMIGELVGGVIANSLAINTDALHMLTDLNLTALMLSSKSPKRF 172

Db 57 KLCIAVVLCLVFMSEVVGKANSALITDAHLSDVAFAISLSLWAAAGWEATPRQ 116

Qy 173 TFGFRLRLVLSAMISLVLYILMGLFLYEAQVORTIHMYEINGDIMLITAAVGVANNVIM 232

Db 117 TYGFRIELGALVSIQLIWLTLGLVYEAIRIVTSEVNGPLMFLVAAGLVNIM 176

Qy 233 GFLNQS-----GHRHSHSLPSNSPT-----RGSGCERNHQD----- 267

Db 177 AVLLGHDRHGSHGHGHGHHNHSRGVTTTHHHHDEHGHSHGHGDKHHAQDVT 236

Qy 268 -----SLAVRAAFVHALGDLVQSVGLIAAYIIRFKPEYKIADPIC 308

Db 237 EQLDKSTQVAKEKRNINLQAVLHVLGDSIQSVGVNIGGAILIWNPEKIVDLIC 296

Qy 309 TYVFSLLVAFTTFRINDTVIILGVPSHLNVYDIKEALMKIEDVYSVEDLNWLSLTS 368

Db 297 TLAFSVILGTTINIRNILEVMESTPREIDATKLEKGLLEMEEVAVHETLWITVG 356

Qy 369 KSTALVHQLIPGSSKWEVQSKANHLNLTNFGYRCITIQLO 411

Db 357 KYLLACHVNIREFADA--DMVLNVIDYIRREYNISHVTIQIE 397

RESULT 6

A84696
probable zinc transporter [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: A84696

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: A84696

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-385 <STO>

A/Cross-references: GB:AE002093; NID:g3980394; PIDN:AAC95197.1; GSPDB:GN00139

C/Genetics:

A/Gene: At2g29410

A/Map position: 2

Query Match 24.5%; Score 534; DB 2; Length 385;

Best Local Similarity 32.4%; Pred. No. 1.3e-35;

Matches 122; Conservative 92; Mismatches 120; Indels 42; Gaps 9;

Qy 69 LOADDSDLLDQDLP-LTNSQLSLKVDSC-----DNC-----SKQREILKORKVKARLTIAAV 119

Db 19 LKPDDBEEMESPSPSKTEENLGVFLSCAFTQEHCVSETKERE-----ESTRRLSLIF 73

Qy 120 LYLFWIGELVGGYIANSIAINTDALHMLTDLNLTALMLSSKSPKRFKFTGPHRL 179

Db 74 LYLIVMSVQIVGFGKANSIAVNTDAHLSDVAGLCVSLAIAKVSSEANPNSFGFKRL 133

Qy 180 EYLSAMISVLLVYILMGLFLYEAQVORTIHMYEINGDIMLITAAVGVANNVIMGELL--N 237

Db 134 EVLAAPLSVQLIWLIVSGVYIIHEAIOIILSRSEVNGEIMFGISAFGFNNLWMLWLGHN 193

Qy 238 QSGHRHSHSLPSN-----SPTRGSCCERNHQD--SLAVRAAPV 276

Db 194 HSHHHHHHHHHHKKHQHHKHEVAAEEMENPLKG---EKSSSKEMNINICQAYL 250

Qy 277 HALGDLVQSVGLIAAYIIRFKPEYKIADPICTYVFSLLVAFTTFRITWDTVIVILEGVP 336

Db 251 HAWADMISQIGVNIIGGIIWVKWLVLDLICTLIFSALAAATLPIKNIIFILMERVP 310

Qy 337 SHLNVDYIKEALMKIEDVYSVEDLNWLSLTSKSTAIHQLIPGSSKWEVQSKANHL 396

Db 311 RMDIEKLERGLKRDGVKIVYDLHWETVGRIVLSCHILPEPGASPK--EITGVNRF 368

Qy 397 LNTFGYRCITIQLOS 412

Db 369 CRKSYGIYHATVOVES 384

RESULT 7

T49164
zinc transporter-like protein - Arabidopsis thaliana

N/Alternate names: protein T20N10.160

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C/Accession: T49164

R/D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; I

submitted to the Protein Sequence Database, April 2000

A/Reference number: Z25017

A/Accession: T49164

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-378 <DAN>

A/Cross-references: EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.160

A/Experimental source: cultivar Columbia; BAC clone T20N10

C/Genetics:

A/Gene: ATSP:T20N10.160

A/Map position: 3

Query Match 24.4%; Score 532; DB 2; Length 378;

Best Local Similarity 33.6%; Pred. No. 1.8e-35;

Matches 108; Conservative 79; Mismatches 110; Indels 24; Gaps 3;

Qy 113 RTIAAVLYLLFMIGELVGGYIANSIAINTDALHMLTDLNLTALMLSSKSPKRF 172

Db 58 KLLIAVLLCAIFIVNEVVGKANSIAITDAHLSDVAFAISLSLWASGKANPOQ 117

Qy 173 TFGFRLRLVLSAMISLVLYILMGLFLYEAQVORTIHMYEINGDIMLITAAVGVANNVIM 232


```
QY 106 KQKVKARLTAAVLYLLEFMIGELVGYIANSLAINTDALHMLTDLISAILLTLLALWLSS 165
Db 3 REKSLKV-LAFSFLIIFLPAFIPLFGLGLTNSLALLSDAGHMLTDAVSIALVAQYLAL 61
QY 166 KSPTRFTFGFHRLEVLMSISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGV 225
Db 62 KVKTKRTTYGLYRLVLAALVNGVFLGLLIGYIILEAIHR--PENPEPKPMYIYAFAG 119
QY 226 VANNVINGFLLNQSGHRHSHSLPNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVOS 285
Db 120 LVLNVLVGYIL-----LKHSEENINIKSALLHVATDTLGS 154
QY 286 VGVLIAAIIIRFKPEYKIADPCTYVFSLLVAFVTFRIIMDTVVIILEGVPSHLNVDIYK 345
Db 155 VAAIIAGIAIVFKFY-LADPILLSVAVALILPSAYSVIKETVNVLLVAPSHINTEELE 213
QY 346 EALMKIEDVVSVDLNTWSITGSKSTAIVHILQIPGSSSKWEVQSKANHL-----LN 399
Db 214 KELNLQGVGVHDLHWSITPGTEVLTVHVW-----EDTSCINDILKEVEKIAH 264
QY 400 TFGMYRCTIQLQSVROQVDRTCANC 424
Db 265 KYGIKHTVQL-----EKEGYACAC 285

RESULT 11
AG1396
cation transport protein (efflux) homolog lmo2575 [imported] - Listeria monocytogenes (s
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AG1396
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Etian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ck, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1396
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97946.1; PID:gl6415256; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2720
C;Superfamily: zinc transporter Znt-2

Query Match 17.7%; Score 387; DB 2; Length 303;
Best Local Similarity 29.2%; Pred. No. 8.1e-24;
Matches 88; Conservative 75; Mismatches 110; Indels 28; Gaps 4;

QY 111 KARLTAAVLYLLEFMIGELVGYIANSLAINTDALHMLTDLISAILLTLLALWLSSKSPK 170
Db 21 KKSLSFISFILLATFVWVEVIGINTNSLALLSDAGHMLSDAVALGLSLAAAFKGEKAASS 80
QY 171 RFTGFRHLEVLMSISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNV 230
Db 81 DKTYGKRFELAAFLNGTLVGISVFIFYEAGIFDFPPQVIGAGMMTI-SVIGLLINI 139
QY 231 IMGFLNQSGHRHSHSLPNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGLI 290
Db 140 LVANIL-----MKGDTSENLMNSAFHLVGLDGLSGVGAIT 175
QY 291 AAYIIRFKPEYKIADPCTYVFSLLVAFVTFRIIMDTVVIILEGVPSHLNVDIYKEALMK 350
Db 176 AALLIIFL-GWNIADPIASVIVAALILVSGWRVLKDAIHILMEGKPNVDTTEIKTFQ 234
QY 351 IEDVYSVEDLNTWSITGSKSTAIVHILQIPGSSSKWEVQSKANHLNTFGMYRCTIQL 410
Db 235 QDGVEVHDLHVWATSDFNALHTV--AEDADKLTIDIEHYLQENFSLHSTIQL 292

RESULT 13
H64810
yBGR protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession: H64810
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Petra, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64810
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-313 <BLAT>
```

```
QY 106 KQKVKARLTAAVLYLLEFMIGELVGYIANSLAINTDALHMLTDLISAILLTLLALWLSS 165
Db 3 REKSLKV-LAFSFLIIFLPAFIPLFGLGLTNSLALLSDAGHMLTDAVSIALVAQYLAL 61
QY 166 KSPTRFTFGFHRLEVLMSISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGV 225
Db 62 KVKTKRTTYGLYRLVLAALVNGVFLGLLIGYIILEAIHR--PENPEPKPMYIYAFAG 119
QY 226 VANNVINGFLLNQSGHRHSHSLPNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVOS 285
Db 120 LVLNVLVGYIL-----LKHSEENINIKSALLHVATDTLGS 154
QY 286 VGVLIAAIIIRFKPEYKIADPCTYVFSLLVAFVTFRIIMDTVVIILEGVPSHLNVDIYK 345
Db 155 VAAIIAGIAIVFKFY-LADPILLSVAVALILPSAYSVIKETVNVLLVAPSHINTEELE 213
QY 346 EALMKIEDVVSVDLNTWSITGSKSTAIVHILQIPGSSSKWEVQSKANHL-----LN 399
Db 214 KELNLQGVGVHDLHWSITPGTEVLTVHVW-----EDTSCINDILKEVEKIAH 264
QY 400 TFGMYRCTIQLQSVROQVDRTCANC 424
Db 265 KYGIKHTVQL-----EKEGYACAC 285

RESULT 11
AG1396
cation transport protein (efflux) homolog lmo2575 [imported] - Listeria monocytogenes (s
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AG1396
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Etian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ck, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1396
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00653.1; PID:gl6412063; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2575
C;Superfamily: zinc transporter Znt-2

Query Match 17.9%; Score 391; DB 2; Length 303;
Best Local Similarity 29.2%; Pred. No. 3.8e-24;
Matches 88; Conservative 76; Mismatches 109; Indels 28; Gaps 4;

QY 111 KARLTAAVLYLLEFMIGELVGYIANSLAINTDALHMLTDLISAILLTLLALWLSSKSPK 170
Db 21 KKSLSFISFILLATFVWVEVIGINTNSLALLSDAGHMLSDAVALGLSLAAAFKGEKAASS 80
QY 171 RFTGFRHLEVLMSISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNV 230
Db 81 DKTYGKRFELAAFLNGTLVGISVFIFYEAGIFDFPPQVIGAGMMTI-SVIGLLINI 139
QY 231 IMGFLNQSGHRHSHSLPNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGLI 290
Db 140 LVANIL-----MKGDTSENLMNSAFHLVGLDGLSGVGAII 175
QY 291 AAYIIRFKPEYKIADPCTYVFSLLVAFVTFRIIMDTVVIILEGVPSHLNVDIYKEALMK 350
Db 176 AALLIIFL-GWNIADPIASVIVAALILVSGWRVLKDAIHILMEGKPNVDTTEIKTFQ 234
QY 351 IEDVYSVEDLNTWSITGSKSTAIVHILQIPGSSSKWEVQSKANHLNTFGMYRCTIQL 410
Db 235 QDGVEVHDLHVWATSDFNALSALTVCEDADR--DKILADIEHYLQENFSLHSTIQL 292
```

[illegible]

```

search completed: July 29, 2004, 17:44:50
Job time: 18 secs

```

Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 17:42:05 ; Search time 19 Seconds
(without alignments)
1165.660 Million cell updates/sec

Title: US-10-024-652-2570

Perfect score: 2183

Sequence: 1 MAGSGAWKRLKSLMRDDAP.....LQSYRQEVDRTCANQSSSP 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	718.5	32.9	372	4	US-10-162-012-40
2	555	25.4	398	3	US-09-461-474-17
3	549	25.1	448	3	US-09-461-474-8
4	536.5	24.6	474	3	US-09-461-474-10
5	484.5	22.2	349	3	US-09-461-474-12
6	447	20.5	322	4	US-10-162-012-42
7	418.5	19.2	359	4	US-09-134-001C-5618
8	372.5	17.1	342	4	US-09-134-001C-4190
9	371	17.0	323	4	US-09-328-352-6181
10	369.5	16.9	320	4	US-09-489-039A-13157
11	368	16.9	520	4	US-09-252-991A-17058
12	344.5	15.8	308	4	US-09-543-681A-5795
13	295	13.5	504	4	US-09-461-325-332
14	295	13.5	504	4	US-10-012-542-332
15	288	13.2	363	4	US-09-328-352-4930
16	285	13.1	490	4	US-09-461-325-158
17	285	13.1	490	4	US-10-012-542-158
18	285	13.1	507	4	US-09-795-927-10
19	250.5	11.5	157	3	US-09-461-474-14
20	209.5	9.6	307	4	US-09-461-325-331
21	209.5	9.6	307	4	US-10-012-542-331
22	199.5	9.1	293	4	US-09-461-325-233
23	199.5	9.1	293	4	US-10-012-542-233
24	188.5	8.6	167	4	US-09-134-001C-2857
25	177.5	8.1	210	4	US-09-252-991A-30886
26	164.5	7.5	348	4	US-09-107-532A-5255
27	140	6.4	165	4	US-08-858-207A-520

ALIGNMENTS

RESULT 1

US-10-162-012-40

; Sequence 40, Application US/10162012

; Patent No. 6682597

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Silos-Santiago, Inmaculada

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS

; FILE REFERENCE: 10448-190001

; CURRENT APPLICATION NUMBER: US/10/162,012

; CURRENT FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: US 60/209,845

; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: US 09/875,321

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: PCT/US01/18340

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US 60/209,257

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: US 09/875,423

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/US01/18398

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/209,238

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: US 09/875,363

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/US01/18247

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/227,068

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: US 09/928,530

; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: PCT/US01/35475

; PRIOR FILING DATE: 2001-08-15

; PRIOR APPLICATION NUMBER: US 60/226,770

; PRIOR FILING DATE: 2000-08-21

; PRIOR APPLICATION NUMBER: US 09/934,421

; PRIOR FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: PCT/US01/26096

; PRIOR FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: US 60/279,281

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: US 10/109,029

; PRIOR FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: PCT/US02/09728

; PRIOR FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: US 60/290,288

; PRIOR FILING DATE: 2001-05-11

Sequence 5023, Ap
Sequence 25117, A
Sequence 3257, Ap
Sequence 8124, Ap
Sequence 22091, A
Sequence 5999, Ap
Sequence 59, Appl
Sequence 4617, Ap
Sequence 3700, Ap
Sequence 409, App
Sequence 5171, Ap
Sequence 5908, Ap
Sequence 12247, A
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 66, Appl

4 US-09-543-681A-5023
4 US-09-252-991A-25117
4 US-09-540-236-3257
4 US-09-328-352-8124
4 US-09-252-991A-22091
4 US-09-328-352-5999
2 US-08-676-279-59
4 US-09-543-681A-4617
4 US-09-134-001C-3700
4 US-09-711-164-409
4 US-09-134-001C-5171
4 US-09-328-352-5908
4 US-09-489-039A-12247
1 US-08-153-848-24
3 US-09-299-843A-24
4 US-09-088-337B-24
5 PCT-US93-11153-24
3 US-09-299-843A-66

6.1 316 4
5.8 372 4
5.6 266 4
5.5 443 4
5.4 302 4
5.4 343 4
5.4 549 2
5.0 493 4
4.9 154 4
4.9 567 4
4.7 311 4
4.6 128 4
4.5 325 4
4.5 359 1
4.5 359 3
4.5 359 4
4.5 359 5
4.5 378 3

28 134
29 126
30 123
31 121
32 117.5
33 117.5
34 117.5
35 110
36 107.5
37 107
38 102
39 101.5
40 99
41 99
42 99
43 99
44 99
45 99

PRIOR APPLICATION NUMBER: US (not assigned)
PRIOR FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 372
TYPE: PRT
ORGANISM: Homo sapiens
US-10-162-012-40

Query Match 32.9%; Score 718.5; DB 4; Length 372;
Best Local Similarity 38.8%; Pred. No. 9.1e-73;
Matches 150; Conservative 88; Mismatches 118; Indels 31; Gaps 7;

QY 56 EAPRRP-VNGAHPLOADDLSLLQD---LPLTNSQLSKL-----VDSCNCKSQRE-- 103
DB 2 EAKEKQHLDDTRPAIRSYTSGLWQEGAGWPLPRPGLDQAIELAAQSNHHCHCAQGPDS 61
QY 104 --ILKQKRVKARLTIAAVLYLLFMIGELVGYIANSIAIMTDALHMLTDLAISAILTLALL 161
DB 62 HCDEPKGKACRQLYVAISAICLLFMIGEVGYLAHSLAVMTDAHLLTDFASMLISLFL 121
QY 162 WLSKSPKTRTFGFHLEVLVSAMISVLLVYILMGFLLYEAVORTIHMNYEINGDMLIT 221
DB 122 WMSRPATKTNFQWQRAEILGALVSLSIWWVTGVLVLAVERLSGDYEIDGGTMLIT 181
QY 222 AAVGVAVNVIMGFLLNQSRRHSHSLSPNSPTRSGCERNHGQDSLAVRAAFVHALGD 281
DB 182 SGCAVAVNIMGLTLHQSGHSHGTT-----NQCEENPSVRAAFIHVIGD 227
QY 282 LVQSVGVLIAYIIRFPEYKIADPCTIYVFSLLVATFTFRILIWDTVVILLEGVPSHLNV 341
DB 228 FMQSGMLVAAIILYFPEYKYVDPICTFVFSILVGTTLTILRDVILVMEGTPTKGVDF 287
QY 342 DYKEALMKIEDVYSVEDLNISLTSKSTAIVHIQILPGSSKWEVQSKANHLILNTF 401
DB 288 TAVEDLLSVGEVREALSHLWALTVAQPVLSVHIAIAQNTDA--QAVLKTASSRLOGKF 345
QY 402 GMYRCTIQLQSYREVDRTCANQSSS 428
DB 346 HFHTVTIQIEDYSDM-KDCQACQGPS 371

RESULT 2
US-09-461-474-17
; Sequence 17, Application US/09461474
; Patent No. 6278042
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Plant Metal Transporters
; FILE REFERENCE: BB1303 US NA
; CURRENT APPLICATION NUMBER: US/09/461,474
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 60/112,562
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-461-474-17

Query Match 25.4%; Score 555; DB 3; Length 398;
Best Local Similarity 33.8%; Pred. No. 4e-54;
Matches 116; Conservative 74; Mismatches 107; Indels 46; Gaps 4;

QY 113 RLTAAYLYLLFMIGELVGYIANSIAIMTDALHMLTDLAISAILTLALLWLSKSPKTRF 172
DB 57 KLCIAVVLCLVFSVEVVGKANSIAITLDAHLLSDVAAFAISLFLSVAAGWEATPQ 116

QY 173 TEGPHRLEVLAMISVLLVYILMGFLLYEAVORTIHMNYEINGDMLITAAVGVAVNVIM 232
DB 117 TYGFRILGALVSIQILWLTGLVYEAIRIVTETSEVNGFLMFLVAAGLVNIIIM 176
QY 233 GFLNQS-----GHRHSHSHSLSPNSPT-----RSGCERNHGQD----- 267
DB 177 AVLLGHGHHGSHGHGHGHHNHSHGVTVTTHHHHHDHGHSHGHGHGDKHHAHGDVT 236
QY 268 -----SLAVRAAFVHALGDVQSVGVLIAYIIRFPEYKIADPIC 308
DB 237 EQLLDKSTQVAAKEKRNINLOAYLHVLDGDSIQSVGMIGGAILWYNPEWKLVDLIC 296
QY 309 TVVFSLLVATFTFRILIWDTVVILLEGVPSHLNVDIKEALMKIEDVYSVEDLNISLTS 368
DB 297 TLAFSVIVLTGTTINIRNILEVMESTPREIDATKLEKGLLEMEVAVVAVHELWALTIVG 356
QY 369 KSTAIVHIQILPGSSKWEVQSKANHLILNTFMYRCTIQLQ 411
DB 357 KVLACHVNIRPEADA--DMVLNKVIDYIRREYNISHVTIQIE 397

RESULT 3
US-09-461-474-8
; Sequence 6, Application US/09461474
; Patent No. 6278042
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Plant Metal Transporters
; FILE REFERENCE: BB1303 US NA
; CURRENT APPLICATION NUMBER: US/09/461,474
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 60/112,562
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Zea mays
US-09-461-474-8

Query Match 25.1%; Score 549; DB 3; Length 448;
Best Local Similarity 29.6%; Pred. No. 2.4e-53;
Matches 133; Conservative 90; Mismatches 146; Indels 80; Gaps 9;

QY 32 SDEAGDE---GLSRFNKLRVVVADDGSEAPERPVNGAHPITLQADDDSLLDQDLPLTNSQL 88
DB 9 SRELGSSEWGLELENLRRSTQKDSMESH---NPSHSOI-----AEVTMDIAASASGA 59
QY 89 S-----LKVDSCD--NCSKQREILKQKVKAR-LTIAAVLYLLFMIGELVGYIANSIAIM 141
DB 60 AGSKFCGKAACDFSDASNSKDAERASMRKLIIVAVVLCVVFVAVVWVGIGKANSAIL 119
QY 142 TDAHMLTDLISAILTLIALWLSKSPKTRTFGFHRLVLSAMISVLLVYILMGFLLYE 201
DB 120 TDAHLLSDVAAFAISLFLSVAAGWEATPROSYGFFRVEILGALVSIQLIWLLAGILVYE 179
QY 202 AVQRTIHMNYEINGDMLITAAVGVAVNVINGFLNQS-----GHRHSHSH----- 247
DB 180 AVVALGSGDVGRSLMFAVSAFGLAVNLVAVLLHGHGHGHGHGHGHGHGHGHGDS 239
QY 248 -----SLPNSPTRSGCER 262
DB 240 DDGSHHDDDEQGRVHHHGHGGAITVTHHHHHHHHDHVEEALIKHEGTQSAGRAG 299
QY 263 NHGQDSIAVRAAFVHALGDVQSVGVLIAYIIRFPEYKIADPCTIYVFSLLVATFTFR 322
DB 300 KKPARNINVSHAYLHVLDGDSVQSVGMVGGAILWIWPEWKEVIDLICITLVFSVVLFTIR 359
QY 323 LIWDTVVILLEGVPSHLNVDIKEALMKIEDVYSVEDLNISLTSKSTAIVHIQILPGS 382

```
Db 360 MLRSILVLMESTPREIDATRLSGLCMGVVAVHHLHWAITVGKVLACHVTTIARDA 419
Qy 383 SSKWEVQSKANHLNLTGMYRCTIQLO 411
Db 420 DA--DEILDVKVIGIKTYNISHVTIQVE 446

RESULT 4
US-09-461-474-10
; Sequence 10, Application US/09461474
; Patent No. 6278042
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Plant Metal Transporters
; FILE REFERENCE: B01303 US NA
; CURRENT APPLICATION NUMBER: US/09/461,474
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 60/112,562
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-461-474-10

Query Match 24.6%; Score 536.5; DB 3; Length 474;
Best Local Similarity 28.5%; Pred. No. 6.9e-52;
Matches 109; Conservative 89; Mismatches 119; Indels 65; Gaps 3;

Qy 93 DSCDNCQKREILKQKVKARLTIAAVLYLLFMIGELVGVYANSIAIMTDALHMLTDL 152
Db 93 DFDSDSSNSKDARBERMASMRKLIIVILCIIFNAVEVGVGKANSAILTDAAHLLSDVA 152
Qy 153 AIITLIALWLSKSPKRTFFGHRLEVLVSAMISLVLLVILMGLFLYEAVQRTIHNYE 212
Db 153 AFAISLFLWAAGWEATPQOSYGFRIEILGALVSIQILWLLAGILVYEAIVLINESGE 212
Qy 213 INGIMLITAAVGVANVINGFLNQSS---GHRHSHSHSLPNSPTRGSCERNHGQD-- 267
Db 213 VQSLMFAVSAGFLFVNII MAVLLGHGDHGHGHGHGHGHGHGHGHGHGHGHGHGH 272
Qy 268 -----SL 269
Db 273 HGVHHHEDHGNSITVNLHHHPGTGHHHDAEBFLKSDAGCDSTQSGADAKAKARNI 332
Qy 270 AVRAAFVHALGVQSVGLIAAVIIRFKPEYKIADPCTVPSLLVAFTFRIIWDTVV 329
Db 333 NVHSAYLVLDGSIQSGVMIGGALIWYKPEWKIIDICTLIFSVIVLFTIKMLNILE 332
Qy 330 IILEGVPSHLNVYIKALKMKIEDVYVEDINWLSLTKGKSTAIHVHQLIPGSSKWEV 389
Db 393 VLMESTPREIDATSLNGLRMDMGVAVHHLHWAITVGKVLACHVTTIQDADA--DQM 450
Qy 390 QSKANHLNLTGMYRCTIQLO 411
Db 451 LDKVIGYIKSYNISHVTIQIE 472

RESULT 5
US-09-461-474-12
; Sequence 12, Application US/09461474
; Patent No. 6278042
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Plant Metal Transporters
; FILE REFERENCE: B01303 US NA
; CURRENT APPLICATION NUMBER: US/09/461,474
```

```
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 60/112,562
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Glycine max
US-09-461-474-12

Query Match 22.2%; Score 484.5; DB 3; Length 349;
Best Local Similarity 28.6%; Pred. No. 3.4e-46;
Matches 99; Conservative 80; Mismatches 106; Indels 61; Gaps 4;

Qy 125 MIGELVGVYANSIAIMTDALHMLTDLISAIIITLIALWLSKSPKRTFFGHRLEVL 184
Db 5 MTEVVVGGIKANSAILTDAAHLLSDVASFAISLFLWAAGWEATPQOSYGFRIEILGA 64
Qy 185 MISVLLVILMGLFLYEAVQRTIHNYEINGDIMLITAAVGVANVINGFL--NQ 238
Db 65 LVSIQMIWLLAGILVYEAIDRIIAGPKNVGDFLVSAGFLVNVNIMALLLGHGHHRH 124
Qy 239 SGHRHSHSHSLPNSP--TRGSGCERNHGQD----- 267
Db 125 AGHSHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGH 184
Qy 268 -----SLAVRAAFVHALGVQSVGLIAAVIIRFKPEYKIAD 305
Db 185 HXEVTELLLGESKGGTKKKQKNVINVOGAYLHVLGDSIQSGVMIGGAVIWNPRQIVD 244
Qy 306 PICTVPSLLVAFTFRIIWDTVVILSGVPSHLNVYIKALKMKIEDVYVEDINWLSL 365
Db 245 LCTLIFSVIVMGTINMLNILEVMENTPREIDATKLERGLDMDVAVHHLHWA 304
Qy 366 TSGKSTAIHVHQLIPGSSKWEVQSKANHLNLTGMYRCTIQLO 411
Db 305 TVGKVLACHVKIRREADA--DLVLDKVIDIKRYVYNISHVTIQIE 348

RESULT 6
US-10-162-012-42
; Sequence 42, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
```

```
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-162-012-42

Query Match      20.5%; Score 447; DB 4; Length 322;
Best Local Similarity 33.8%; Pred. No. 5.4e-42;
Matches 112; Conservative 75; Mismatches 102; Indels 42; Gaps 8;

QY 116 IAAVLLFELMIGELVGVYANSIAIMTDALHMLTDLTSAIILTLALWLSKSPKPTFTG 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 ISLAALLMLIKLIGVLSLALADALHSLSVASSLSIALRLAEKPFDEKHPFG 62

QY 176 FHRLEVSAMI-SVLLVYILMGFLLYEAVORTIHMYEINGDMLIT----- 221
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 HHRAETLAALNSVFLVIVSLYEALIERLISPDYEIPDAVLAADIMEPEBEPGLFEV 122

QY 222 --AAVGAVN-----VIMGFLNQSGRHSHSLPNSPTRSGCERNHQDLSAVRAA 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 GGVALGVALGTALVLLGLVNNALHG-----LRRVG-KKLKSEHNLAVRAA 170

QY 275 FVHALGDLVOSGVLIAAYIRFK-----PYKIADPCTYVFSLLVAFTRFIIMDT 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 ALHVLGDLSSVGLIAALLIYFTGYSFGKWKWYVADPIASILSIILYTAFLKES 230

QY 328 VWILEGVPSHLVD-YIKALMKIEDVYVEDLNISLTSKSTAIHVLIQIIPGSSK- 385
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 VLILLEGTPSKEDLERIKKTLISIPGVKGVDLHIWYLGNSKFIASVHVVEDNDLDKE 290

QY 386 WEEVQSKANHLLNTFGMYRCTIQLQSYROE 416
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 AHDLIAIERELHKLKFGIEHVTVHVEPASEE 321

RESULT 7
US-09-134-001C-5618
; Sequence 5618, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 416
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4190

Query Match      17.1%; Score 372.5; DB 4; Length 342;
Best Local Similarity 26.9%; Pred. No. 1.8e-33;
Matches 86; Conservative 88; Mismatches 119; Indels 27; Gaps 5;

QY 111 KARLTAAVLLFELMIGELVGVYANSIAIMTDALHMLTDLTSAIILTLALWLSKSPK 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 KKLWFSFIISLFWLVEIIGFVANSALLSDGFMLSDAISUGVALIAFIYAEKATK 106

QY 171 RFTFGFHRLEVSAMISVLLVYILMGFLLYEAVORTIHMYEINGDMLITAAVAVNV 230
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 SKTYGKRFELAAFLNGVTLFIISIIITEAIRPLEPP-EVQSKEMFIISVIGLMVNI 165

QY 231 IMGFLNQSGRHSHSLPNSPTRSGCERNHQDLSAVRAAFVHALGDLVQSVGLI 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 166 IVAILMFKGG-----DTSH-----NLNRRGAFHLVGLDFGSGVAIV 202
```

```
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5618
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5618

Query Match      19.2%; Score 418.5; DB 4; Length 359;
Best Local Similarity 27.8%; Pred. No. 1.1e-38;
Matches 85; Conservative 87; Mismatches 109; Indels 25; Gaps 3;

QY 107 QRKVKARLTAAVLLFELMIGELVGVYANSIAIMTDALHMLTDLTSAIILTLALWLSK 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 QSSSKITLWLSLVITMIFTVVFGGIVSNSALLSDGFMLSDLVALGLSVAIYFSSK 122

QY 167 SPTKRFTFGFHRLEVSAMISVLLVYILMGFLLYEAVORTIHMYEINGDMLITAAVGV 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 PPTKNTYTGFLRLIIVAFNLGLALIVISLIGIMYEGIMRIIHPR-PVESGMILIAFI 181

QY 227 AVNVIMGFLNQSGRHSHSLPNSPTRSGCERNHQDLSAVRAAFVHALGDLVQSV 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 TANIVLTILMISLKK-----ENNINIQSALWHFIDGLLNSL 218

QY 287 GVLIAAYIIRPKPEYKIADPCTYVFSLLVAFTRFIIMDTVVIILGVPSHLVDYIKE 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 GIIVAFVLIHF-TGWNIVDPIISLILRGGYKIKKASKVLMERVDPDYDTDEIMG 277

QY 347 ALMKIEDVYVEDLNISLTSKSTAIHVLIQIIPGSSKWEVQSKANHLLNTFGMYRC 406
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 278 AMKQVEGVIDIHPEFLMSVTINQSLSAHVLSDDYIKSPYATINKVSDLLKTOYGLEHV 337

QY 407 TIQLQS 412
   : : : :
Db 338 TLQIEN 343

RESULT 8
US-09-134-001C-4190
; Sequence 4190, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4190
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4190

Query Match      17.1%; Score 372.5; DB 4; Length 342;
Best Local Similarity 26.9%; Pred. No. 1.8e-33;
Matches 86; Conservative 88; Mismatches 119; Indels 27; Gaps 5;

QY 111 KARLTAAVLLFELMIGELVGVYANSIAIMTDALHMLTDLTSAIILTLALWLSKSPK 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 KKLWFSFIISLFWLVEIIGFVANSALLSDGFMLSDAISUGVALIAFIYAEKATK 106

QY 171 RFTFGFHRLEVSAMISVLLVYILMGFLLYEAVORTIHMYEINGDMLITAAVAVNV 230
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 SKTYGKRFELAAFLNGVTLFIISIIITEAIRPLEPP-EVQSKEMFIISVIGLMVNI 165

QY 231 IMGFLNQSGRHSHSLPNSPTRSGCERNHQDLSAVRAAFVHALGDLVQSVGLI 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 166 IVAILMFKGG-----DTSH-----NLNRRGAFHLVGLDFGSGVAIV 202
```

```

Qy 291 AAVIIKPKPEYKIADPICMYVFSLLVAFTFPIIWDTVIILEGVPSHLNVDIKEALMK 350
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 ASDLI-WGFNFTIADPIASILVSLIKLSAYGISKSLNLMIEGTPNDIDLNVIKAISK 261
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 351 IEDVYSVEDLNTKSLTSGSTAIVHIQILPGSSSKWEVQSKANHLILNTFGMYRCTIQL 410
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 DERIQNHCHVWITISNDNALSCHAVPEYLSVOTCTMLKSIIESDLLQNLNIORHTIQL 321
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 411 QS--YRQVEDRTCANQSSS 428
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 ETPEKHDESTLCSGIHERS 341
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-328-352-6181
; Sequence 6181, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6181
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6181

```

```

Query Match          17.0%; Score 371; DB 4; Length 323;
Best Local Similarity 29.4%; Pred. NO. 2.4e-33;
Matches      92; Conservative    68; Mismatches 117; Indels   36; Gaps     5;

QY  113 RLIIAAVYLIFLGMIGELGVGYIANSIAIMTDLAHMLTDLSAIIILTLLALWSSSKPTKRF 172
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::
26  KLIILALATTFIVFIEVIAGLTQSIALUSDAAHFTDARALAIALVAIQISKPADNKR 85
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::

QY  173 TFGFHRLEVLISAMISVLVYILMGFLFXEAVORTIHMYNEINGDIMLITAAVGVAENVIM 232
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::
86  TFCYQRFEILALFNALMFVVAIYILXEAYIR-FSQPPEIQSGVGLIVATIGLVINLIS 144
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::

QY  233 GFILNSGGRHSISHSLPSNPSTRGSCGRNHGQDSLAVRAAFVHALGDVLQSVGVLIAA 292
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::
145 MKILMSAN-----NSLVKGAYLEVLSDALGSGVGI GA 179
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::

QY  293 YIIRFEPXYKIADPICTYVFSLVAPTFRITDVTWIILEGVPSHLVNDVIKEALMKIE 352
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::
180 IIFYTNWYI-DTLAVIGFWLPRTVWLKQSNILLGVPDEVIEDIKLRADLLSIN 238
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::

QY  353 DVYSVEDLNWSLTSGKSTAIVHIQLPGSSSKWEVOSKANHLHLNTFGMYRTCICLQGS 412
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::
239 GVSSIHQLKWAITSKNIIHLTVHLPAPEADRNK---LYQDAVEMLSHHGIGEVTLQIE- 294
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::

QY  413 YRQEBVBTCANCO 425
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::
295 -----DDAEINCO 302
Db   :|||:|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::

RESULT 10
US-09-489-039A-13157
Sequence 13157, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747

```

```
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13157
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13157

Query Match          16.9%; Score 369.5; DB 4; Length 320;
Best Local Similarity 29.8%; Pred.No. 3.5e-33;
Matches 99; Conservative 76; Mismatches 118; Indels 41; Gaps 9;

Qy      79 QDLPLTNSQLSLKVDSCDCKSQREILKQKVKAULTIAAVLYLFLFMIGELVGGYIANSL 138
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      3 RDOTMAHSHSHSSVQAPDNSNAR-----RLTWAFIVTAGFMLTEAVGGAISGSL 51

Qy     139 AINTDALHMLTDLSAILLTLLALNLWSKSPTKFPGFHRLEVLNSLMISVLLVIIMGLF 198
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     52 ALLADAGHMLTDSAAULFALLAVFASRPENRAHTFGWLRLTTLAFLNAIALWVTIMLI 111

Qy     199 LYEA VORTIHMYEINGDIIMLTITAAVGVAANNVMISFLLNQSQRHSHSHSLSPSTRGS 258
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    112 VWBAIQEFQHPO--PVAGVTMMVITAVAGLLANLVAFWIL---HRGSE----- 153

Qy     259 GCERNHGQDSLAVRAAFVIALGDVLQSVGVLTIAAYTIIRFKPEYKIADPCTVFSLLVAF 318
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    154 --ERN-----LNVRAAALHVGLDGLSGVAIAVAAYI-LTTGWTPVDPILSVLVSCVLR 205

Qy     319 TTRFIWTDTVIIILEGVPGHINVDYIKCALMK-IEDVYSVEDLINWSLTSGKSTAIWHIQ 377
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    206 SANWLLKESLINELEGAPRSLDVAAALQDRIRSIPEVRDVHHVHW-LVGEKFPVMTLHVQ 264

Qy     378 LIFGSSSKVEEVOSKANHLILLNTFGMYRCTIQLQ 411
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    265 VWPDPDH--DALLNRILHFLEHKYEIAHAATVOME 296
```

RESULT 11
 US-09-252-991A-17058
 ; Sequence 17058, Application US/09252991A
 ; Patent NO. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 17058
 ; LENGTH: 520
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-17058

Query Match	16.9%	Score 368;	DB 4;	Length 520;
Best Local Similarity	29.3%;	Pred. No. 1.2e-32;		
Matches 93; Conservative	72;	Mismatches 116;	Indels 36;	Gaps 6;
QY	113	RLTAAVLYLLFMIGELVGGYIANSIAIMTDALHMLTDSAILITLALWLSEKSPTKRF	172	
Dd	237	RLKWALLTGSLFAEVVGILTGSLAISDAAHMLTDAVALAIALAAINAIARRPTNDRL	296	
QY	173	TGCFHRLEVLASAMISLVLLVMGLFLYEAVQSTITHNNVEINGDIMLTAAVGVANNVIM	232	
Dd	297	TYGHRFEILLAAFNAPNALLFGVAFYILYAAYER-LNQPAETIQSGMLVI AVLGLVNLIAS	355	
QY	233	GFLNQGHRRHSLSHPNSPTRGSCCERNHQDLSLAVERAAFHALGDLIVQSQVGLIAA	292	

Db 356 MRL-----APAQ-----NSLVKAGYLEVWSMDLGLGVIAA 390
Qy 293 YIIRPKPKYKADPCTVYVSLVAFTTFRIMDTVILLEGVSHLVNDYIKEALMKIE 352
Db 391 IVIRP-TGAWVDSLVAVLIGFWLPRTWILLCSFLVLEGVPEKIQALREALIGIP 449
Qy 353 DVYVEDINISLNGSKSTAIVHQLIPGSSSKKEEVQSKANHLNLTFGMYRCTIQLQS 412
Db 450 GTVGLDHUWVITSGKLSLGLVDPALVDA-EALGTVVALLDHRYEIEHSTIQLQ- 507
Qy 413 YRQVEDRTCANCQSSSP 429
Db 508 -----TSACAQAEPP 517

RESULT 12

US-09-543-681A-5795
; Sequence 5795, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5795
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5795

Query Match 15.8%; Score 344.5; DB 4; Length 308;
Best Local Similarity 29.1%; Pred. No. 2.3e-30;
Matches 88; Conservative 67; Mismatches 118; Indels 29; Gaps 4;
Qy 111 KARLTIAVLLFMIGELVGGYIANSIAIMTDALHMLTDLTAIITLLALWLSKSPK 170
Db 25 ESRLLIAFALGTGSEWIEFGYLTESLALISDAWMTDPAFALLALIAHAGRAADL 84
Qy 171 RFTGFHRLVLSAMISVLLVYILMGFLYEAQVORTIHMNYEINGDMLITAAVGVAVNV 230
Db 85 FRTGYARFETIAAAMNALILMAVAFILYEAQR-LSSPPDICSMGLVVAIAGLIINF 143
Qy 231 IMGFLNQSGHRHSHSLPSNSTRGSGCERNHGODSLAVRAAFVHALGDLVQSVGLI 290
Db 144 ISMKMLTSA-----KDESLNVKAGYLEVWADMGLSGVVI 178
Qy 291 AAYIIRPKPKYKADPCTVYVSLVAFTTFRIMDTVILLEGVSHLVNDYIKEALMK 350
Db 179 GAVIIL-WLTGQLVDSIIAVLIGFWPPTWILLKECLNILEGVPKGINLTVETDINN 237
Qy 351 IEDVYVEDINISLNGSKSTAIVHQLIPGSSSKKEEVQSKANHLNLTFGMYRCTIQL 410
Db 238 TAGVASSHDHLWALTOSKILSHIVYQPNVDS--ETRLAIDKQLREQFHINHTLQM 295
Qy 411 QS 412
Db 296 ES 297

RESULT 13

US-09-461-325-332
; Sequence 332, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A

; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 332
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (403)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-332

Query Match 13.5%; Score 295; DB 4; Length 504;
Best Local Similarity 23.4%; Pred. No. 2.3e-24;
Matches 99; Conservative 76; Mismatches 124; Indels 124; Gaps 13;
Qy 105 LKQKVKARLTIAVLLFMIGELVGGYIANSIAIMTDALHMLTDLTAIITLLALWLS 164
Db 3 IRHERNGRLLCMLATFMFMVLEVVSRTVSSSLMLSDSFHMLSDVLALVALVAERFA 62
Qy 165 SKS-PTKFTGFHRLVLSAMISVLLVYILMGFLYEAQVORTIHMNYEINGDMLITAA 223
Db 63 RRTATQKNTGWTAEVAGALVNAIFLTGLCPAILLEAIEFTIEPHEMQQPLVVLGV 122
Qy 224 VGVAVNV-----MGFLNQSGHRHS-----HSHSLP----- 250
Db 123 AGLLVNLGLCLFHHSGF-SQDSCHXSHGCHGHGLPKGPRVKSTRPGSSDINVAPG 181
Qy 251 -----SNS-----PTRGSGC-----ERNH----- 264
Db 182 BQPPQETNTLVANTSNGLKLPDADPENRSGDTEVQVQVGNLVREPDHMELEEDRA 241
Qy 265 QGDSLAVERAAAFVHALGDLVQSVGLIAAYIIRF-----KPEYKI- 303
Db 242 GQ--LNMKGVLFLVGLDGLGSIIVVNAIVFYFSWKGCSEGDGFCVPCFPDCKPFBV 299
Qy 304 -----ADPCTVYVSLVAFTTFRIMDTVILLEGVSHLVNDYIKE 346
Db 300 NSTHASYEAGPCWVLYLDPTLCVMMVCILTYTPLLKESALILLQTVPRQIDIRNLK 359
Qy 347 ALMKIEDVYVEDINISLNGSKSTAIVHQLIPGSSSKKEEVQSKANHLNLTFGMYRC 406
Db 360 ELRNVEGVVEVHELHWQLAGSRIIATAHIKCEDPTS--YMEV-AKKIKDVFNHGHIAH 416
Qy 407 TIQ 409
Db 417 TIQ 419

RESULT 14

US-10-012-542-332
; Sequence 332, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:

Blank Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 17:37:14 ; Search time 54 Seconds
(without alignments)
2244.683 Million cell updates/sec

Title: US-10-024-652-2570
Perfect score: 2183
Sequence: 1 MAGSGHWKRLKMLRKDDAP.....LQSYRQVDRTCANQSSSP 429

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2183	100.0	429	5	ABG61811 Prostate
2	2183	100.0	429	5	ABJ17930 Zinc tran
3	2183	100.0	429	5	ABJ17931 Zinc tran
4	2183	100.0	429	5	ABJ17933 Zinc tran
5	2183	100.0	438	5	Aae24062 Human pro
6	2179	99.8	429	5	ABJ17932 Zinc tran
7	2179	99.8	429	5	ABJ17934 Zinc tran
8	2179	99.8	429	7	Aae38600 Human zin
9	2166.5	99.2	430	7	ADB2764 Human pro
10	747	34.2	358	5	ABB3085 Transport
11	739	33.9	326	6	ABU52726 Human int
12	723	33.1	356	6	ABU54543 Human NOV
13	722.5	33.1	372	5	Aae32905 Human tra
14	722.5	33.1	372	5	ABB3084 Human tra
15	718.5	32.9	372	6	ABU99884 Human cat
16	679	31.1	323	6	ABU54544 Human NOV
17	653.5	29.9	369	5	ABG60224 Human zin
18	652.5	29.9	472	4	ABG60324 Drosophil
19	648.5	29.7	369	5	ABG60226 Human tra
20	648	29.7	320	4	ABG60094 Human tra
21	648	29.7	320	5	Aau99907 Human 842
22	648	29.7	320	5	Aae17562 Human pan
23	638	29.2	320	4	ABU52725 Human int
24	617.5	28.3	422	5	ABG60225 Human zin
25	616	28.2	388	7	ADC77681 Human 443

26	599.5	27.5	1677	4	ABB69976	Abb69976 Drosophil
27	555	25.4	344	3	AAG43479	Aag43479 Arabidops
28	555	25.4	344	3	AAG22264	Aag22264 Arabidops
29	555	25.4	398	3	AAG43478	Aag43478 Arabidops
30	555	25.4	398	3	AAG22263	Aag22263 Arabidops
31	549	25.1	448	4	AAE09321	Aae09321 Maize zin
32	538.5	24.7	322	5	ABP69136	Abp69136 Human pol
33	536.5	24.6	474	4	AAE09322	Aae09322 Rice zinc
34	534	24.5	375	3	AAG31822	Aag31822 Arabidops
35	534	24.5	385	3	AAG31821	Aag31821 Arabidops
36	532	24.4	452	4	ABB65511	Abb65511 Drosophil
37	530	24.3	274	7	ADB65759	Adb65759 Human pro
38	525	24.0	330	3	AAG22265	Aag22265 Arabidops
39	525	24.0	330	3	AAG43480	Aag43480 Arabidops
40	524.5	24.0	359	3	AAG31823	Aag31823 Arabidops
41	523.5	24.0	420	6	ABP72086	Abp72086 Perennial
42	484.5	22.2	349	4	AAE09323	Aae09323 Soybean z
43	447	20.5	322	5	Aau99928	Aau99928 Human 842
44	447	20.5	322	5	AAU99931	Aau99931 Human 850
45	439.5	20.1	319	6	ABW72087	Abw72087 Staphyloc

ALIGNMENTS

RESULT 1

ABG61811
ID ABG61811 standard; protein; 429 AA.
XX
AC ABG61811;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated protein #12.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX
OS Mammalia.
XX
PN WO200230268-A2
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-02639572.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
(EOSB-) EOS BIOTECHNOLOGY INC.
XX
Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
WPI: 2002-471335/50.
N-PSDB; ABK92126.

Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue.

Claim 27; Page 310; 436pp; English.

The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-

CC associated polynucleotides (designated PC genes) that selectively
 CC hybridise to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABG61800-ABG61944 represent prostate cancer-associated proteins
 XX
 SQ Sequence 429 AA;

Query Match 100.0%; Score 2183; DB 5; Length 429;
 Best Local Similarity 100.0%; Pred. No. 2.1e-234;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFSDAGDEGLSRFNKLRVVVADGSEAPER 60
 DB 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFSDAGDEGLSRFNKLRVVVADGSEAPER 60
 QY 61 PVNGAHTPLQADDDSLDDQLPLTNSQLSKVDSQKQREILKQKVKARLTAAVL 120
 DB 61 PVNGAHTPLQADDDSLDDQLPLTNSQLSKVDSQKQREILKQKVKARLTAAVL 120
 QY 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLISAILTLALWLSKSPKRTFFGFHRL 180
 DB 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLISAILTLALWLSKSPKRTFFGFHRL 180
 QY 181 VLSAMISVLLVYILMGFLLYEAQVORTIHMYEINGDMLITAAVGVAVNVIMGFLNQSG 240
 DB 181 VLSAMISVLLVYILMGFLLYEAQVORTIHMYEINGDMLITAAVGVAVNVIMGFLNQSG 240
 QY 241 HRHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAVYIRFKPE 300
 DB 241 HRHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAVYIRFKPE 300
 QY 301 YKIADPCTYVFSLLVAFTTFRITWDTVWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 DB 301 YKIADPCTYVFSLLVAFTTFRITWDTVWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 QY 361 NIWLSLTSKSTAIWHIQLIFGSSSKWEVOSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
 DB 361 NIWLSLTSKSTAIWHIQLIFGSSSKWEVOSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
 QY 421 CANCQSSSP 429
 DB 421 CANCQSSSP 429

RESULT 2

ABJ17930
 ID ABJ17930 standard; protein; 429 AA.
 AC ABJ17930;
 XX
 XX
 DT 16-JAN-2003 (first entry)
 XX
 XX Zinc transporter protein 108P5H8 v-1.
 DE
 XX
 XX Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
 KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
 KW passive immunisation.
 XX
 XX Unidentified.
 OS
 XX
 XX WO200260953-A2.
 FN
 XX
 XX 08-AUG-2002.
 PD
 XX
 XX 17-DEC-2001; 2001WO-US049133.
 PF

XX 15-DEC-2000; 2000US-0256210P.
 PR (AGEN-) AGENSYS INC.
 XX
 XX Challita-Bid PM, Faris M, Afar DEH, Hubert RS, Mitchell SC;
 PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;
 XX WPI; 2002-627469/67.
 DR N-PSDB; AAL53482.
 XX
 XX Composition comprising a substance that modulates the status of a zinc
 PT transporter protein (108P5H8), useful in diagnosing and treating patients
 PT with cancer that express 108P5H8, such as breast, colon, ovarian or lung
 PT cancer.
 XX
 XX Claim 33; Fig 2A; 309pp; English.
 PS
 XX The invention relates to a new composition comprising a substance that
 CC modulates the status of a zinc transporter protein, designated as
 CC 108P5H8, or a molecule that is modulated by 108P5H8. The composition is
 CC useful in diagnosing, preventing, prognosticating or treating patients
 CC with cancer that expresses 108P5H8, such as breast, colon, ovarian or
 CC lung cancer. The 108P5H8 gene or its fragment can be used to elicit a
 CC humoral or cellular immune response. The antibodies are useful in active
 CC or passive immunisation. The 108P5H8 polynucleotides are useful as probes
 CC and primers for the amplification or detection of 108P5H8 genes, as
 CC coding sequences for directing the expression of 108P5H8 polypeptides, or
 CC as tools for modulating or inhibiting the expression of 108P5H8 genes.
 CC The polynucleotides of the invention can be used to treat disorders by
 CC gene therapy. This sequence represents a zinc transporter protein 108P5H8
 CC sequence of the invention
 XX
 SQ Sequence 429 AA;

Query Match 100.0%; Score 2183; DB 5; Length 429;
 Best Local Similarity 100.0%; Pred. No. 2.1e-234;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFSDAGDEGLSRFNKLRVVVADGSEAPER 60
 DB 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFSDAGDEGLSRFNKLRVVVADGSEAPER 60
 QY 61 PVNGAHTPLQADDDSLDDQLPLTNSQLSKVDSQKQREILKQKVKARLTAAVL 120
 DB 61 PVNGAHTPLQADDDSLDDQLPLTNSQLSKVDSQKQREILKQKVKARLTAAVL 120
 QY 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLISAILTLALWLSKSPKRTFFGFHRL 180
 DB 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLISAILTLALWLSKSPKRTFFGFHRL 180
 QY 181 VLSAMISVLLVYILMGFLLYEAQVORTIHMYEINGDMLITAAVGVAVNVIMGFLNQSG 240
 DB 181 VLSAMISVLLVYILMGFLLYEAQVORTIHMYEINGDMLITAAVGVAVNVIMGFLNQSG 240
 QY 241 HRHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAVYIRFKPE 300
 DB 241 HRHSHSLPSNSTRGSGCERNHGQDSLAVRAAFVHALGDLVQSGVGLIAAVYIRFKPE 300
 QY 301 YKIADPCTYVFSLLVAFTTFRITWDTVWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 DB 301 YKIADPCTYVFSLLVAFTTFRITWDTVWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 QY 361 NIWLSLTSKSTAIWHIQLIFGSSSKWEVOSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
 DB 361 NIWLSLTSKSTAIWHIQLIFGSSSKWEVOSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
 QY 421 CANCQSSSP 429
 DB 421 CANCQSSSP 429

RESULT 3

Seq ID	Accession	Length	Score	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382
--------	-----------	--------	-------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------

```

Query Match      100.0%; Score 2183; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.1e-234;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSGAWRLKSMRLKDDAPLFLNDTSAPFSDSDEAGDEGLSRFNKLRVWVADDCSEAPER 60
DB 1 MAGSGAWRLKSMRLKDDAPLFLNDTSAPFSDSDEAGDEGLSRFNKLRVWVADDCSEAPER 60
QY 61 PVNGAHPPTLQADDDSLDDPLTNLSQLSLKVDSCDNCCKOREILKORKVKARLTIAAVL 120
DB 61 PVNGAHPPTLQADDDSLDDPLTNLSQLSLKVDSCDNCCKOREILKORKVKARLTIAAVL 120
QY 121 YLLFMIGELVGGYTANSLAINTDALHMLTDLSAIILTLALWLSKSPTRKFTFGFHRLE 180
DB 121 YLLFMIGELVGGYTANSLAINTDALHMLTDLSAIILTLALWLSKSPTRKFTFGFHRLE 180
QY 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
DB 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
QY 241 HRHSHSLPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300
DB 241 HRHSHSLPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300
QY 301 YKIADPCTYVFSLLVAFTTFRITWDTWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
DB 301 YKIADPCTYVFSLLVAFTTFRITWDTWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
QY 361 NIWLSGKSTAIVHIQILPGSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
DB 361 NIWLSGKSTAIVHIQILPGSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
QY 421 CANCQSSSP 429
DB 421 CANCQSSSP 429

RESULT 5
RAE24062
ID AAE24062 standard; protein; 438 AA.
XX AC AAE24062;
XX DT 23-SEP-2002 (first entry)
XX DE Human prostate specific protein (PSP) #5.
XX KW Human; prostate specific protein; PSP; prostate specific nucleic acid;
XX KW vaccine; transgenic; prostate cancer; gene therapy; transgenic animal;
XX KW PSNA.
XX OS Homo sapiens.
XX FN WO200224718-A1.
XX PD 28-MAR-2002.
XX PF 19-SEP-2001; 2001WO-US029386.
XX PR 19-SEP-2000; 2000US-0233746P.
XX FA (DIAD-) DIADEXUS INC.
XX PI Sun Y, Recipon H, Caferkey R, Ali S;
XX DR WPI; 2002-471216/50.
XX PT Novel isolated prostate specific polypeptide useful for identifying,
XX PT diagnosing, monitoring, staging, imaging, and treating prostate cancer
XX PT and non-cancerous disease states in prostate.
XX PS Claim 37; Page 198-199; 210pp; English.

```

```

XX The invention relates to prostate specific proteins (PSP) and prostate
XX specific nucleic acids (PSNA). Sequences of the invention are useful for
XX identifying, diagnosing, monitoring, staging, imaging and treating
XX prostate cancer and non-cancerous disease states in prostate. They are
XX also useful for producing engineered prostate tissue for treatment and
XX research. The PSNA sequences are used in gene therapy and for producing
XX transgenic animals and cells. The invention is also used as vaccines. The
XX present sequence is human prostate specific protein of the invention
XX Sequence 438 AA;
SQ
Query Match      100.0%; Score 2183; DB 5; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.2e-234;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSGAWRLKSMRLKDDAPLFLNDTSAPFSDSDEAGDEGLSRFNKLRVWVADDCSEAPER 60
DB 1 MAGSGAWRLKSMRLKDDAPLFLNDTSAPFSDSDEAGDEGLSRFNKLRVWVADDCSEAPER 60
QY 61 PVNGAHPPTLQADDDSLDDPLTNLSQLSLKVDSCDNCCKOREILKORKVKARLTIAAVL 120
DB 61 PVNGAHPPTLQADDDSLDDPLTNLSQLSLKVDSCDNCCKOREILKORKVKARLTIAAVL 120
QY 121 YLLFMIGELVGGYTANSLAINTDALHMLTDLSAIILTLALWLSKSPTRKFTFGFHRLE 180
DB 121 YLLFMIGELVGGYTANSLAINTDALHMLTDLSAIILTLALWLSKSPTRKFTFGFHRLE 180
QY 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
DB 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
QY 241 HRHSHSLPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300
DB 241 HRHSHSLPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300
QY 301 YKIADPCTYVFSLLVAFTTFRITWDTWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
DB 301 YKIADPCTYVFSLLVAFTTFRITWDTWIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
QY 361 NIWLSGKSTAIVHIQILPGSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
DB 361 NIWLSGKSTAIVHIQILPGSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
QY 421 CANCQSSSP 429
DB 421 CANCQSSSP 429

RESULT 6
ABJ17932
ID ABJ17932 standard; protein; 429 AA.
XX AC ABJ17932;
XX DT 16-JAN-2003 (first entry)
XX DE Zinc transporter protein 108P5H8 v-3.
XX KW Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
XX KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
XX KW passive immunisation.
XX OS Unidentified.
XX FN WO200260953-A2.
XX PD 08-AUG-2002.
XX PF 17-DEC-2001; 2001WO-US049133.
XX PR 15-DEC-2000; 2000US-0256210P.
XX PS

```

PA (AGEN-) AGENSYS INC.
XX Challita-Bid PM, Faris M, Afar DEH, Hubert RS, Mitchell SC;
PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;
XX WPI; 2002-627469/67.
DR N-PSDB; AAL53484.
XX Composition comprising a substance that modulates the status of a zinc
PT transporter protein (108PSH8), useful in diagnosing and treating patients
PT with cancer that express 108PSH8, such as breast, colon, ovarian or lung
PT cancer.
XX Claim 33; Fig 2C; 309pp; English.
PS
XX The invention relates to a new composition comprising a substance that
CC modulates the status of a zinc transporter protein, designated as
CC 108PSH8, or a molecule that is modulated by 108PSH8. The composition is
CC useful in diagnosing, preventing, prognosticating or treating patients
CC with cancer that expresses 108PSH8, such as breast, colon, ovarian or
CC lung cancer. The 108PSH8 gene or its fragment can be used to elicit a
CC humoral or cellular immune response. The antibodies are useful in active
CC or passive immunisation. The 108PSH8 polynucleotides are useful as probes
CC and primers for the amplification or detection of 108PSH8 genes, as
CC coding sequences for directing the expression of 108PSH8 polypeptides, or
CC as tools for modulating or inhibiting the expression of 108PSH8 genes.
CC The polynucleotides of the invention can be used to treat disorders by
CC gene therapy. This sequence represents a zinc transporter protein 108PSH8
CC sequence of the invention
XX
SQ Sequence 429 AA;

Query Match 99.8%; Score 2179; DB 5; Length 429;
Best Local Similarity 99.8%; Pred. No. 5.9e-234;
Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGGAWKRLKSMRKDDAPLNDTSAPFSDGDEGLSRFNKLRVWVADGSEAPER 60
Db 1 MAGGAWKRLKSMRKDDAPLNDTSAPFSDGDEGLSRFNKLRVWVADGSEAPER 60

Qy 61 PVNGAHTLQADDDSLDQDLPLTNSQLSKVDCNCSKQREILKQKVKARLTIAAVL 120
Db 61 PVNGAHTLQADDDSLDQDLPLTNSQLSKVDCNCSKQREILKQKVKARLTIAAVL 120

Qy 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALWLSKSPTKRFTFGFHRLE 180
Db 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALWLSKSPTKRFTFGFHRLE 180

Qy 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
Db 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240

Qy 241 HRHSHSLPNSPTRGSGCERNHGQSLAVRAAFVHALGDLVQSVGLIAAYIIRKPE 300
Db 241 HRHSHSLPNSPTRGSGCERNHGQSLAVRAAFVHALGDLVQSVGLIAAYIIRKPE 300

Qy 301 YKIADPCTYVFSLLVAFTFRILWDVTWIILEGVPSHLNVDIYKEALMKIEDVYSVEDL 360
Db 301 YKIADPCTYVFSLLVAFTFRILWDVTWIILEGVPSHLNVDIYKEALMKIEDVYSVEDL 360

Qy 361 NIWLSLTKSTAIWHIOLIPGSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
Db 361 NIWLSLTKSTAIWHIOLIPGSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420

Qy 421 CANCQSSSP 429
Db 421 CANCQSSSP 429

RESULT 7
ID ABJ17934
XX

AC ABJ17934;
XX 16-JAN-2003 (first entry)
XX Zinc transporter protein 108PSH8 v-3 #2.
DE
XX Cytostatic; gene therapy; vaccine; zinc transporter protein 108PSH8;
KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
KW passive immunisation.
XX Unidentified.
OS
XX WO200260953-A2.
FN
XX 08-AUG-2002.
PD
XX 17-DEC-2001; 2001WO-US049133.
PF
XX 15-DEC-2000; 2000US-0256210P.
PR
XX (AGEN-) AGENSYS INC.
PA
XX Challita-Bid PM, Faris M, Afar DEH, Hubert RS, Mitchell SC;
PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;
XX WPI; 2002-627469/67.
DR
XX Composition comprising a substance that modulates the status of a zinc
PT transporter protein (108PSH8), useful in diagnosing and treating patients
PT with cancer that express 108PSH8, such as breast, colon, ovarian or lung
PT cancer.
XX Disclosure; Fig 3B; 309pp; English.
PS
XX The invention relates to a new composition comprising a substance that
CC modulates the status of a zinc transporter protein, designated as
CC 108PSH8, or a molecule that is modulated by 108PSH8. The composition is
CC useful in diagnosing, preventing, prognosticating or treating patients
CC with cancer that expresses 108PSH8, such as breast, colon, ovarian or
CC lung cancer. The 108PSH8 gene or its fragment can be used to elicit a
CC humoral or cellular immune response. The antibodies are useful in active
CC or passive immunisation. The 108PSH8 polynucleotides are useful as probes
CC and primers for the amplification or detection of 108PSH8 genes, as
CC coding sequences for directing the expression of 108PSH8 polypeptides, or
CC as tools for modulating or inhibiting the expression of 108PSH8 genes.
CC The polynucleotides of the invention can be used to treat disorders by
CC gene therapy. This sequence represents a zinc transporter protein 108PSH8
CC sequence of the invention
XX
SQ Sequence 429 AA;

Query Match 99.8%; Score 2179; DB 5; Length 429;
Best Local Similarity 99.8%; Pred. No. 5.9e-234;
Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGGAWKRLKSMRKDDAPLNDTSAPFSDGDEGLSRFNKLRVWVADGSEAPER 60
Db 1 MAGGAWKRLKSMRKDDAPLNDTSAPFSDGDEGLSRFNKLRVWVADGSEAPER 60

Qy 61 PVNGAHTLQADDDSLDQDLPLTNSQLSKVDCNCSKQREILKQKVKARLTIAAVL 120
Db 61 PVNGAHTLQADDDSLDQDLPLTNSQLSKVDCNCSKQREILKQKVKARLTIAAVL 120

Qy 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALWLSKSPTKRFTFGFHRLE 180
Db 121 YLLFMIGELVGGYIANSIAIMTDALHMLTDLAISAILTLALWLSKSPTKRFTFGFHRLE 180

Qy 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
Db 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240

Qy 241 HRHSHSLPNSPTRGSGCERNHGQSLAVRAAFVHALGDLVQSVGLIAAYIIRKPE 300
Db 241 HRHSHSLPNSPTRGSGCERNHGQSLAVRAAFVHALGDLVQSVGLIAAYIIRKPE 300

Qy 301 YKIADPCTYVFSLLVAFTFRILWDVTWIILEGVPSHLNVDIYKEALMKIEDVYSVEDL 360
Db 301 YKIADPCTYVFSLLVAFTFRILWDVTWIILEGVPSHLNVDIYKEALMKIEDVYSVEDL 360

Qy 361 NIWLSLTKSTAIWHIOLIPGSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420
Db 361 NIWLSLTKSTAIWHIOLIPGSSSKWEVQSKANHLNLTFGMYRCTIQLQSYRQEVDR 420

Qy 421 CANCQSSSP 429
Db 421 CANCQSSSP 429

RESULT 7
ID ABJ17934
XX

Db 241 HHHSHSLPSNSTRGSGCERNHQDLSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300
 QY 301 YKIADPICYVFSLLVAFTRIIWDTVIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 Db 301 YKIADPICYVFSLLVAFTRIIWDTVIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 QY 361 NIWSLTSGKSTAIHVIQIIPGSSSKWEVOSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
 Db 361 NIWSLTSGKSTAIHVIQIIPGSSSKWEVOSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
 QY 421 CANCQSSSP 429
 Db 421 CANCQSSSP 429
 RESULT 8
 AAE38600
 ID AAE38600 standard; protein; 429 AA.
 AC AAE38600;
 DT 04-DEC-2003 (first entry)
 DE Human zinc transporter 4 protein.
 KW Human; urological disorder; urinary incontinence; gene therapy; cancer;
 KW kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;
 KW urethra; overflow urinary incontinence; stress urinary incontinence;
 KW nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;
 KW zinc transporter 4.
 OS Homo sapiens.
 PN WO2003061573-A2.
 PD 31-JUL-2003.
 PP 16-JAN-2003; 2003WO-US001450.
 PR 18-JAN-2002; 2002US-0349511P.
 PR 28-FEB-2002; 2002US-0360500P.
 PR 15-MAR-2002; 2002US-0365041P.
 PR 19-APR-2002; 2002US-0374063P.
 PR 14-AUG-2002; 2002US-0403468P.
 PR 27-SEP-2002; 2002US-0414262P.
 PR 21-OCT-2002; 2002US-0419986P.
 PR 05-NOV-2002; 2002US-0423809P.
 PR 26-NOV-2002; 2002US-0429797P.
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Silos-Santiago I, Karicheti V;
 DR N-PSDB; AAD58501.
 PT Identifying a compound for treating urological disorders, for example
 PT urinary incontinence by assaying the ability of the compound to modulate
 PT the nucleic acid expression or polypeptide activity.
 XX Disclosure; Page 217-218; Opp; English.
 CC The present relates to a method for identifying a compound for treating
 CC urological disorders e.g., urinary incontinence including overactive/
 CC oversensitive bladder, overflow urinary incontinence, stress urinary
 CC incontinence caused by dysfunction of the bladder, urethra or central or
 CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
 CC cancer of the prostate or kidney disorders. The method is also useful for
 CC modulating hyperplasia in a cell and treating a subject having a
 CC urological disorder. The invention is also used in gene therapy. The
 CC present sequence is human zinc transporter 4 protein
 XX Sequence 429 AA;

Query Match 99.8%; Score 2179; DB 7; Length 429;
 Best Local Similarity 99.8%; Pred. No. 5.9e-234;
 Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFSDSDEAGDEGLSRFNKRLRVVAVDDGSEAPER 60
 Db 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFSDSDEAGDEGLSRFNKRLRVVAVDDGSEAPER 60
 QY 61 PVNGAHTPLQADDDSLDDQDPLTNSQLSLKVDSCDNCCKOREILKQKVKARLTIAAVL 120
 Db 61 PVNGAHTPLQADDDSLDDQDPLTNSQLSLKVDSCDNCCKOREILKQKVKARLTIAAVL 120
 QY 121 YLLFMIGELVGYTANSLAINTDALHMLTDLSAIILTLLALWLSKSPKTKFTFGFHRLE 180
 Db 121 YLLFMIGELVGYTANSLAINTDALHMLTDLSAIILTLLALWLSKSPKTKFTFGFHRLE 180
 QY 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
 Db 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQSG 240
 QY 241 HHHSHSLPSNSTRGSGCERNHQDLSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300
 Db 241 HHHSHSLPSNSTRGSGCERNHQDLSLAVRAAFVHALGDLVQSGVLIAAYIIRFKPE 300
 QY 301 YKIADPICYVFSLLVAFTRIIWDTVIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 Db 301 YKIADPICYVFSLLVAFTRIIWDTVIILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 QY 361 NIWSLTSGKSTAIHVIQIIPGSSSKWEVOSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
 Db 361 NIWSLTSGKSTAIHVIQIIPGSSSKWEVOSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
 QY 421 CANCQSSSP 429
 Db 421 CANCQSSSP 429
 RESULT 9
 ADB82764
 ID ADB82764 standard; protein; 430 AA.
 AC ADB82764;
 DT 04-DEC-2003 (first entry)
 DE Human protein sequence useful for the treatment of cancer (SeqID 1545).
 KW human; prostate; cancer; cytostatic; gene therapy; vaccine;
 KW immune response.
 OS Homo sapiens.
 PN WO2003050236-A2.
 PD 19-JUN-2003.
 PP 04-SEP-2002; 2002WO-US028214.
 PR 07-DEC-2001; 2001US-00012697.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 PI Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
 PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;
 PI Garcia V, Jones LW, Stache-Crain B, Scott EW;
 DR WPI; 2003-513972/48.
 PT New polynucleotides derived from human prostate, useful for modulating
 PT immune response to prevent or treat cancer.

PS	Claim 18; SEQ ID NO 1545; 188pp; English.	
XX	This invention relates to novel isolated polynucleotides of human origin, particularly isolated from the human prostate. Specifically, it refers to the diagnostics and therapeutics comprising these novel human polynucleotides, and includes the derived probes, antisense oligonucleotides and antibodies thereof. The identification of these human prostate genes that can inhibit tumour growth is useful for understanding the progression and nature of complex diseases such as cancer, and hence they are important in the drug discovery process. The present invention describes these polynucleotides and encoded polypeptides as exhibiting cytostatic activity, and through gene therapy and/or vaccines they can be used to modulate the immune response for the prevention or treatment of cancers, particularly of the prostate, but also for breast, lung and colon cancer. This polypeptide sequence is a human protein sequence useful for the treatment of cancer, used in an exemplification of the invention. NOTE: These sequences are not given in the specification but are provided on the WIPO website.	
XX		
SQ	Sequence 430 AA;	
	Query Match 99.2%; Score 2166.5; DB 7; Length 430;	
	Best Local Similarity 99.5%; Pred. No. 1.5e-232;	
	Matches 428; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	
QY	1 MAGSGAWKRLKMLRKDAPLFLNDTSAPFSDGDEGLSRFNKLRVWVADDSSEAPER 60	
Db	1 MAGSGAWKRLKMLRKDAPLFLNDTSAPFSDGDEGLSRFNKLRVWVADDSSEAPER 60	
QY	61 PVNGAHTLQADDSDLLDQDLPLTNSQLSLKVDSCNCSKQRIILKQKVKALTTAAVL 120	
Db	61 PVNGAHTLQADDSDLLDQDLPLTNSQLSLKVDSCNCSKQRIILKQKVKALTTAAVL 120	
QY	121 YLLPMIGELVGGYIANGSLAETDHALHMLTDLASAILLTLLALWLSKSPTRFTFGHRL- 179	
Db	121 YLLPMIGELVGGYIANGSLAETDHALHMLTDLASAILLTLLALWLSKSPTRFTFGHRLG 180	
QY	180 EVLSAMISLVLLVYLMGFLYEAQVORTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQS 239	
Db	181 XVLASAILSVLLVYLMGFLYEAQVORTIHMNYEINGDIMLITAAVGVAVNVIMGFLNQS 240	
QY	240 GHRHSHSLPSPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAYIIRFKP 299	
Db	241 GHRHSHSLPSPNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAYIIRFKP 300	
QY	300 EYKTADPTCTVFESLLVAFTRIIWDTVVIILEGVPSHLNVDYIKEALMKIEDVYSVED 359	
Db	301 EYKTADPTCTVFESLLVAFTRIIWDTVVIILEGVPSHLNVDYIKEALMKIEDVYSVED 360	
QY	360 LNIWLSLTSKSTAIVHIQLIPGSSSKWEYVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 419	
Db	361 LNIWLSLTSKSTAIVHIQLIPGSSSKWEYVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 420	
QY	420 TCANCQSSSP 429	
Db	421 TCANCQSSSP 430	
	RESULT 10	
AB883085	ID AB883085 standard; protein; 358 AA.	
XX		
AC	AB883085;	
XX		
DT	02-OCT-2002 (first entry)	
XX	Transporter related protein.	
XX		
KW	Rat; transporter protein; zinc transporter; pharmacogenomic analysis;	
KW	diagnosis; drug screening; gene therapy.	
XX		
OS	Rattus norvegicus.	
XX		

PN	WO200224910-A2.	
XX		
PD	28-MAR-2002.	
XX		
PF	20-SEP-2001; 2001WO-US029218.	
XX		
FR	20-SEP-2000; 2000US-0234160P.	
PR	19-OCT-2000; 2000US-00691219.	
XX		
PA	(PEXE) PE CORP NY.	
XX		
PI	Wei M, Ketchum KA, Di Francesco V, Beasley EM;	
XX		
WPI	2002-404954/43.	
XX		
PT	Novel human transporter proteins, related to zinc transporter subfamily, useful as model for developing human therapeutic targets and serves as target for human therapeutics.	
PT		
XX		
PS	Disclosure; Page 75; 75pp; English.	
XX		
CC	The invention relates to an isolated human transporter protein that is related to the zinc transporter subfamily. Polynucleotides and polypeptides of the invention are useful for treating a disease or condition mediated by human transporter protein. The protein also provide a target for diagnosing a disease or predisposition to disease mediated by the peptide, and in pharmacogenomic analysis. The peptides are also useful for treating a disorders characterised by absence of, inappropriate or unwanted expression of the protein. The nucleic acids are also useful in drug screening assays and as a target for treatment by the compounds identified through drug screening. The invention also provides vectors for gene therapy in patients with aberrant expression of the gene encoding the transporter protein. The gene of the invention has been found to be expressed in humans in the kidney, testis, heart, placenta, small intestine and liver. The current sequence represents a rat amino acid sequence that is relative to the transporter protein of the invention	
XX		
SQ	Sequence 358 AA;	
	Query Match 34.2%; Score 747; DB 5; Length 358;	
	Best Local Similarity 42.0%; Pred. No. 5.2e-74;	
	Matches 148; Conservative 78; Mismatches 108; Indels 18; Gaps 4;	
QY	82 PRTNSQLSKVDSCNCSKQRI-----LKQKVKARLTIAAVLYLLFMIGELVGGYIAN 136	
Db	19 PWNLSVELAVQSNHYCHAQKDSGHPNSEKQARARKLYVASAICLVNIGELVGGYLAQ 78	
QY	137 SLAIMTDALHMLTDLASAILLTLLALWLSKSPTRFTFGHRLVLSAMISVLLVYILMG 196	
Db	79 SLAIMTDAAHLITDFASMLISLFLSWSSRPATKTMNFGWQRAEILGALLSVLSIWWVTG 138	
QY	197 FLLYEAQVORTIHMNYEINGDIMLITAAVGVAVNVIMGFLNCSGHRHSHSLPNSPTR 256	
Db	139 VLVYLAQVORLISGDYIEKIGDVTNLTSGCAVAVNIIMGALHQSCHGSHSHSHEUSS--- 195	
QY	257 GSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAYIIRFKPEYKIADPTCTVFESLIV 316	
Db	196 -----QQQNPSVRAAFIHWGDLQSVGVVAAVYIIFKPEYKYVDPTCTFSLIV 248	
QY	317 APTTFRITWDTVVIILEGVPSHLNVDYIKEALMKIEDVYSVEDLNINSLTSKSTAIVHI 376	
Db	249 LGTTILTRILVDILMEGTPKGVDTFTVKNLLSVGDGVLEALHSLHIALTVAQPVLSVHI 308	
QY	377 QLIPGSSSKWEYVQSKANHLLNTFGMYRCTIQLQSYRQEVDRDRTCANCCSSS 428	
Db	309 AIAQNVDA--QAVLKVARDRLOGKFNFTMTIQIESYSEDM-XSCQECQGPS 357	
	RESULT 11	
ABU52726	ID ABU52726 standard; protein; 326 AA.	
XX		


```

XX WPI; 2003-046858/04.
DR N-PSDB; ABX72171.
XX
XX New isolated NOVX polypeptide useful for treating atherosclerosis,
XX metabolic disorders, diabetes, obesity, infectious disease, anorexia,
XX neurodegenerative disorders, Alzheimer's disease and cancer.
XX
XX Claim 1; Page 94; 666pp; English.
XX
XX The invention relates to human polypeptides, termed NOVX, and the
XX polynucleotides encoding them. The polypeptides and polynucleotides are
XX useful for diagnosing disease, and screening for potential therapeutic
XX agents. The sequences are useful for treating metabolic disorders,
XX cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
XX stenosis, atrial septal defect (ASD), atrioventricular canal defect,
XX ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
XX septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma,
XX atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
XX disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
XX hematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
XX and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides
XX of the invention
XX
XX Sequence 356 AA;
XX
XX Query Match 33.1%; Score 723; DB 6; Length 356;
XX Best Local Similarity 40.5%; Pred. No. 2.5e-71;
XX Matches 143; Conservative 82; Mismatches 106; Indels 22; Gaps 4;
XX
XX 81 LPTNSQLSKVDCNCSKQRE-----ILKQKVKARLTIAAVLYLLFMIGLVGYIA 135
XX 20 LPLDLQALIELAAQSNHHCHAKGPDSDHCDPKGKAQQLVVAIAICLLFMIGLVGYLA 79
XX
XX 136 NSIAIMTDALHMLTDLGAILITLALMLWSKSPTRFTFGHLEVLVSAMISVLLVILM 195
XX 80 HSLAVMTDAALHTLDFASMLISLFLSMWSRPAKTNFQWQRAEILGALVSLVWVVT 139
XX
XX 196 GFLLYAVORTIMHNVINGIDIMLTAAVGVAVNVINGFLLNOSGHRHSHSLPSNSPT 255
XX 140 GVLYLAVERLISDYEIDGTMTLTSGCAVAVNMIMGLTHOSGHSHGTT----- 192
XX
XX 256 RGSOCERNHGQDSNAVRAAFVHALGDLVQSVGLIAAYIIRFPEYKIADPITCYVFSLL 315
XX 193 -----NQDENPVSRAAPTHVIGDFWQSMGLVAAVILYFKPEYKVDPICTFVFSIL 245
XX
XX 316 VAPTFRLIWDTVILLEGVPSHLNVDYIKKALMKIEDVYSVEDLMTWSLTSKSTAIYH 375
XX 246 VLGTTLTILRDVILVMEGTPKGVDFFAVRDILLSVEGVSEALHSLHIALTVAPVLSVH 305
XX
XX 376 IQLIPGSSSKWEVQSKANHLLNTFGMYRCTIQLQSYRQEVORTCANQSSS 428
XX 306 IAIQAQNTDA--QAVLKTASSRLQCKFHFTVTIQIEDYSEDH-KDCQACQGPS 355
XX
XX RESULT 13
XX AAEE22905
XX ID AAEE22905 standard; protein; 372 AA.
XX AC AAEE22905;
XX
XX 09-AUG-2002 (first entry)
XX
XX Human transporter and ion channel (TRICH) 4.
XX
XX Human; transporter and ion channel; TRICH; transport disorder;
XX diabetes mellitus; angina; Alzheimer's disease; neurological; epilepsy;
XX stroke; Huntington's disease; meningitis; muscle; myocarditis; cancer;
XX infectious myositis; arrhythmia; asthma; immunological; gene therapy;
XX acquired immunodeficiency syndrome; AIDS; allergy; atherosclerosis;
XX cell proliferative disorder; cerebroprotective; cirrhosis; hepatitis;
XX transgenic; neuroprotective; anticonvulsant; nootropic; cytosstatic;
XX antiinflammatory; hepatototropic; psoriasis.

```

```

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 141..159
XX FT /label= Transmembrane_domain
XX PN WO200222684-A2.
XX
XX PD 21-MAR-2002.
XX
XX 14-SEP-2001; 2001WO-US028938.
XX
XX 15-SEP-2000; 2000US-0232685P.
XX 22-SEP-2000; 2000US-0234842P.
XX 29-SEP-2000; 2000US-0236882P.
XX 05-OCT-2000; 2000US-0239057P.
XX 13-OCT-2000; 2000US-0240540P.
XX 18-OCT-2000; 2000US-0241700P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Lee EA, Yue H, Lal PG, Wallia NK, Baughn MR, Warren BA, Lee S;
XX Sanjanwala MS, Yao MG, Ramkumar J, Thornton M, Gandhi AR;
XX Policky JL, Elliott VS, Arvizu C, Raumann BE, Bruns CM, Naini A;
XX Hafalia AJA, Nguyen DB, Xu V, Lu DAM, Ison CH, Griffin JA;
XX Reddy RM, Burford N;
XX
XX WPI; 2002-393948/42.
XX N-PSDB; AAD36301.
XX
XX Polypeptides of human transporters and ion channels, useful for
XX diagnosing, treating or preventing transport, neurological, muscle,
XX immunological and cell proliferative disorders.
XX
XX Claim 1; Page 144-145; 204pp; English.
XX
XX The invention relates to human transporters and ion channels (TRICH) and
XX their corresponding nucleic acid sequences. TRICH is useful for screening
XX an agonist/antagonist that modulates its activity. TRICH is useful as an
XX immunogen for preparing antibodies which are useful for diagnosing a
XX condition of disease associated with its expression in a subject, and for
XX detecting and purifying it from a sample. TRICH DNA is useful as probe or
XX a primer for assessing toxicity of a test compound. Composition
XX comprising TRICH or its agonist is useful for treating a disease or
XX condition associated with decreased expression of functional TRICH and
XX composition comprising TRICH antagonist is useful for treating a disease
XX or condition associated with TRICH overexpression of TRICH. TRICH
XX sequence is used in the diagnosis and treatment of transport disorder
XX e.g. diabetes mellitus, angina, Alzheimer's disease; neurological
XX disorder e.g. epilepsy, stroke, Huntington's disease, bacterial and viral
XX meningitis, muscle disorder e.g. myocarditis, infectious myositis,
XX arrhythmias, asthma, immunological disorder e.g. acquired
XX immunodeficiency syndrome (AIDS), allergies, atherosclerosis; and cell
XX proliferative disorders e.g. cirrhosis, hepatitis, psoriasis and cancers.
XX TRICH DNA is used in gene therapy. TRICH DNA is useful for creating
XX knockin humanised animals (pigs) or transgenic animals (mice or rats) to
XX model human disease. The present sequence is human TRICH protein
XX
XX Sequence 372 AA;
XX
XX Query Match 33.1%; Score 722.5; DB 5; Length 372;
XX Best Local Similarity 39.0%; Pred. No. 3e-71;
XX Matches 151; Conservative 88; Mismatches 117; Indels 31; Gaps 7;
XX
XX 56 EAPERP-VNGAFTLQADDSDLLDQD---LPTNSQLSKL-----VDCNCSKQRE--- 103
XX 2 EAKERQHLDDAPRAIRSYTGSWQSGAGWIPRFGDLQATELAQAQSNHHCHAKGPS 61
XX
XX 104 --ILKQKVKARLTIAAVLYLLFMIGELVGVVIANSLAIMTDALHMLTDLAISITLAL 161
XX 62 HCDPKKGAQRLQYVASAICLLFMIGVGVVGLAHSIAVMTDAHLLTDFASMLISLPSL 121

```


FT Modified-site /label= Cytoplasmic_domain_2
FT 124..126 /note= "Ser is O-phosphorylated by protein kinase C"
FT Domain 141..163
FT Modified-site /label= Transmembrane_domain_3
FT 143..148 /note= "Gly is N-myristoylated"
FT Region 164..177
FT Domain 178..196
FT Modified-site /label= Transmembrane_domain_4
FT 183..188 /note= "Gly is N-myristoylated"
FT Domain 197..218
FT Modified-site /label= Cytoplasmic_domain_3
FT 199..202 /note= "Histidine-rich"
FT Modified-site /note= "Glycosaminoglycan attachment site"
FT 216..218 /note= "Ser is O-phosphorylated by protein kinase C"
FT Domain 219..243
FT Modified-site /label= Transmembrane_domain_5
FT 233..238 /note= "Gly is N-myristoylated"
FT Region 244..252
FT Domain 253..277
FT Modified-site /label= Transmembrane_domain_6
FT 264..269 /note= "Gly is N-myristoylated"
FT Domain 278..372
FT Modified-site /label= Cytoplasmic_domain_4
FT 280..285 /note= "C-terminal tail"
FT Modified-site /note= "Gly is N-myristoylated"
FT 281..283 /note= "Thr is O-phosphorylated by protein kinase C"
FT Modified-site 338..340 /note= "Ser is O-phosphorylated by protein kinase C"
XX WO200279427-A2.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009728.
XX 28-MAR-2001; 2001US-0279281P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Curtis RAJ;
XX WPI; 2003-046802/04.
XX N-PSDB; ABQ79299.
XX New isolated human cation transporter 84226 polypeptides and nucleic acid
XX molecules, for treating or preventing a disorder of aberrant activity of
XX 84226-expressing cell, e.g. pancreatic cancer or metal transport-related
XX disorder.
XX Claim 5; Page 106-107; 117pp; English.
XX This sequence represents a novel human cation transporter family member,
XX designated 84226. Members of this family of proteins are integral
XX membrane proteins which increase cellular tolerance to divalent metal
XX cations such as zinc, cadmium and cobalt by mediating their diffusion
XX across membranes. Cation transporter 84226 shares the structural features
XX of the cation transporter family, including six transmembrane domains, a
XX histidine-rich loop between the fourth and fifth transmembrane domains, a
XX cation efflux domain, and a long C-terminal tail. Expression analysis
XX indicated that the cation transporter is highly expressed in pancreas and
XX is slightly expressed in heart, kidney, skeletal muscle and small
XX intestine. Cation transporter 84226 nucleic acid molecules and proteins

CC are useful for diagnosing, treating or preventing a disorder
CC characterised by aberrant activity or expression of cation transporter
CC 84226, such as conditions involving metal transport-related disorders;
CC disorders associated with cellular toxicity resulting from aberrant or
CC deficient cation diffusion; pancreatic disorders (e.g., pancreatic cancer
CC or pancreatitis); metabolic disorders (e.g., obesity, anorexia nervosa,
CC cachexia, lipid disorders or diabetes); pain disorders; or aberrant or
CC deficient cellular proliferation or differentiation (e.g., cancers).
CC Cation transporter 84226 molecules are also useful as diagnostic targets
CC and therapeutic agents for controlling cardiovascular disorders (e.g.,
CC hypertension, atherosclerosis, coronary artery disease or arrhythmias),
CC kidney disorders (e.g., amyloidosis, glomerulonephritis or Goodpasture's
CC syndrome), or as pharmacogenomic markers. They may additionally be used
CC in drug screening, and the polynucleotides can be used for chromosome
CC mapping, tissue typing or in forensic biology
XX
XX Sequence 372 AA;
Query Match 32.9%; Score 718.5; DB 6; Length 372;
Best Local Similarity 38.8%; Pred. No. 8.5e-71;
Matches 150; Conservative 88; Mismatches 118; Indels 31; Gaps 7;
QY 56 EAPERP-VNGARPTLQADDSDLLDQD---LPTNSQLSK-----VDSQDCNSKQRE--- 103
DB 2 EAKEQHLLDTPAIRSYTGSILWQSGAGWIPLPFGLDLQAIELAAQSNHHCHQKGPDS 61
QY 104 ---ILKQKVKARLTIAAVLYLLFMIGELVGGVYANSIAIMTDALHMLTDLGAIILTLAL 161
DB 62 HCDPKKGAQRLYVASAICLLFMIGEYVGGYLAHSLAVMTDAHLLTDFASMLISLFSL 121
QY 162 WLSSKSPTKRFTFGPHRLVLSAMISVLLVYLMGLFVLA VORTIHMNYEINGDIMLIT 221
DB 122 WNSSRPATKTMNFGWQRAEILGALVSVLSIWVYGVLYLAVERLISGDYEIDGTMILT 181
QY 222 AAVGVAVNVIMGFLNQSGRHSHSLPSNSPTGSGCERNHGQDSLAVRAAFVHALGD 281
DB 182 SGCAVAVNIIMGLTLHQSGHGHSGTT-----NQOENSPSRAAFTHVIGD 227
QY 282 LVQSGVLTAAYIIEPKPKYKADPICYVPSLAVAFTRITMDTVVILLEGVPSHLNV 341
DB 228 FMQSMGLVAAYILYIKPKYKVDPCICFVFSILVGLTGLTILRDVILVLMGTPKGVDP 287
QY 342 DYIKEALMKIEDVGSVEDINWLSLTSKSTAIHVLIQLIPGSSSKWEVQSKANHLILNTF 401
DB 288 TAVRDLLLSVEGVEALHSLHIWALTVAQPVLSVHIAIAQNTDA--QAVLKTASSRLQKGF 345
QY 402 GMYRCTIQLQSYRQEVDRTCANCQSSS 428
DB 346 HFHTVTIQTIEDYSEDM-KDCQACQGPS 371

Search completed: July 29, 2004, 17:43:09
Job time : 57 secs

Blank sheet